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OM nucleic - nucleic search, using sw model

Run on: June 18, 2005, 06:35:24 ; Search time 4754.26 Seconds
(without alignments)
10548.684 Million cell updates/sec

Title: US-10-623-472-31

Perfect score: 1035

Sequence: 1 atggccaattacacgtgcg.....accattccacgaagtgtaa 1035

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hlg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_ats.*

12: gb_ey.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1035	100.0	1035	6	AX521743 Sequence
2	1035	100.0	1546	9	AF015524 Homo sapi
3	1035	100.0	1547	6	AR526903 Sequence
4	1035	100.0	1790	9	AF015525 Homo sapi
5	1031.8	99.7	1475	6	AX454430 Sequence
6	1031.8	99.7	1475	6	AX490908 Sequence
7	1031.8	99.7	1644	6	CQ714577 Sequence
8	1031.8	99.7	1645	6	CQ882060 Sequence
9	1031.8	99.7	1645	6	AX549068 Sequence
10	1031.8	99.7	1698	9	AF014958 Homo sapi
11	1031.8	99.7	1755	9	BC071682 Homo sapi
12	1031.8	99.7	1770	9	BC025717 Homo sapi
13	1031.8	99.7	143068	6	AX335952 Sequence
14	1031.8	99.7	143068	9	HSU95626 Homo sapien
15	1031.8	99.7	185437	9	AC098613 Homo sapi
16	1030.2	99.5	1035	9	AV337001 Homo sapi
17	1030.2	99.5	1645	9	HSU97123 Homo sapien
18	1029.8	99.5	1270	6	AR270193 Sequence
19	1028.6	99.4	1035	9	HSA344142 Homo sapi

20	973.4	94.0	1050	6	ARI68095	ARI68095	Sequence
21	950.2	91.8	1035	9	AF124381	AF124381	Macaca mu
22	695.8	67.2	7644	6	AX345787	AX345787	Sequence
23	651	62.9	7644	6	AX345786	AX345786	Sequence
24	631	61.0	1195	4	AB119274	AB119274	Sub scrof
25	631	61.0	1314	4	AB119273	AB119273	Sub scrof
26	631	61.0	14233	4	AP006435	AP006435	Sub scrof
27	631	61.0	165558	4	AP006185	AP006185	Sub scrof
28	505.2	48.8	588	6	AX079344	AX079344	Sequence
29	443.2	42.8	231984	2	AC112401	AC112401	Rattus no
30	414	40.0	1790	10	AF316576	AF316576	Mus muscu
31	414	40.0	2045	6	AX454145	AX454145	Sequence
32	414	40.0	2045	10	AF030185	AF030185	Mus muscu
33	414	40.0	169165	10	AC118727	AC118727	Mus muscu
34	414	40.0	230772	10	AC132832	AC132832	Mus muscu
35	412.4	39.8	1083	6	AX521744	AX521744	Sequence
36	412.4	39.8	1182	10	MMU318863	AJ318863	Mus muscu
37	412.4	39.8	1793	10	BC038631	BC038631	Mus muscu
38	412.4	39.8	1858	10	AB009384	AB009384	Mus muscu
39	326.4	31.5	620	6	AR379763	AR379763	Sequence
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41	237.8	23.0	1019	9	AF162000	AF162000	Colobus g
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ALIGNMENTS

RESULT 1	AX521743	Sequence 31 from Patent WO02057779.	1035 bp	DNA	linear	PAT 05-OCT-2002
LOCUS	AX521743					
DEFINITION	Sequence 31 from Patent WO02057779.					
ACCESSION	AX521743					
VERSION	AX521743.1	GI:23572791				
KEYWORDS						
SOURCE						
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1	Boddeke, S.H. and Biber, K.				
AUTHORS						
TITLE	Cloning and expression of a new mcp receptor in glial cells					
JOURNAL	Patent: WO 0205779-A 31 25-JUL-2002;					
	Rijksuniversiteit Groningen (NL)					
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	/note="hCCR12 chemokine receptor sequence"					

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Matches 1035;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
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Db	1	ATGCCCAATTACCGCTGGCACCAGAGGATGAATATGTCCTCATAGAGGTGAACGTG	60			
Qy	61	GAGNGCGATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG	120			
Db	61	GAGNGCGATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG	120			
Qy	121	GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	180			
Db	121	GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	180			
Qy	181	CTTATCTCTGTTAAATATAAAGGACTCAAAACGGGTGGAAATATCTATCTCTTAAACTTG	240			

Db	181	CTTATCCTGTGTAATAATAAGGACTCAAAACGCGTGGAAAATATCTATCTCTAAACTTG	240
Qy	241	GCAGTTCTTAACATTTGTGTTTCTTCGCTTACCCCTGCCCCCTCTGGGCTCATGCTGGGGCGAT	300
Db	241	GCAGTTCTTAACATTTGTGTTTCTTCGCTTACCCCTGCCCCCTCTGGGCTCATGCTGGGGCGAT	300
Qy	301	CCCATGTGTAAAAATTTCTCATTTGGACTGTACTTCTGTGGGCCCTGTACAGTGAGACATTTTTTC	360
Db	301	CCCATGTGTAAAAATTTCTCATTTGGACTGTACTTCTGTGGGCCCTGTACAGTGAGACATTTTTTC	360
Qy	361	AATTGCCCTTCTGACTGTGCAAAGGTACTAGTGTGTTTTTGCACAAGGGCAACTTTTTCTCA	420
Db	361	AATTGCCCTTCTGACTGTGCAAAGGTACTAGTGTGTTTTTGCACAAGGGCAACTTTTTCTCA	420
Qy	421	GCCAGGAGGGGGGCCCTGTGGCATCATTTACAAGTGTCTTGGCATCGGTAAACAGCCATT	480
Db	421	GCCAGGAGGGGGGCCCTGTGGCATCATTTACAAGTGTCTTGGCATCGGTAAACAGCCATT	480
Qy	481	CTGCGCCACTTTTGCCTGGAATTCGTGGTTTATAAACTCAGATGGAAGACCCAGAAATACAAG	540
Db	481	CTGCGCCACTTTTGCCTGGAATTCGTGGTTTATAAACTCAGATGGAAGACCCAGAAATACAAG	540
Qy	541	TGTGCATTTAGCAGAACTCCCTTCTGCGAGCTGATGAGACATTTCTGGAAAGCATTTTTCTG	600
Db	541	TGTGCATTTAGCAGAACTCCCTTCTGCGAGCTGATGAGACATTTCTGGAAAGCATTTTTCTG	600
Qy	601	ACTTTAAAAATGACATTTTGGTCTTGTCTCTCCCTCTATTTATTTTACATTTCTCTAT	660
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Qy	661	GTGCAATAGAAAAACACTAAGGTTCAGGGAGCAGAGGTATAGCCCTTTTCAAGCTTGT	720
Db	661	GTGCAATAGAAAAACACTAAGGTTCAGGGAGCAGAGGTATAGCCCTTTTCAAGCTTGT	720
Qy	721	TTTGCCCGTAATGGTAGTCTTCTCTGATGTGGCGCCCTACAATATTGCAATTTTCTCTG	780
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Db	781	TCCACTTTCAAAGAACACTTCTCCCTGAGTACTGCAAGAGCAGCTACAATCTGGACAAA	840
Qy	841	AGTGTTCACATCACTAAACTCATCGCCACACCCACTGCTGCATCAACCCCTCTCTGTAT	900
Db	841	AGTGTTCACATCACTAAACTCATCGCCACACCCACTGCTGCATCAACCCCTCTCTGTAT	900
Qy	901	CGGTTTCTTGATGGGACATTTAGCAAAATACCTCTGCGCTGTTTTCCATCTCGGTAGTAAC	960
Db	901	CGGTTTCTTGATGGGACATTTAGCAAAATACCTCTGCGCTGTTTTCCATCTCGGTAGTAAC	960
Qy	961	ACCCACTTCAACCCAGGGGCGAGCTGCAACAGGCATCGAGGGAAGAACCTGACCAT	1020
Db	961	ACCCACTTCAACCCAGGGGCGAGCTGCAACAGGCATCGAGGGAAGAACCTGACCAT	1020
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LOCUS	AF015524		
DEFINITION	AF015524	1546 bp mRNA linear	PRI 07-SEP-1998
	AF015524.1	GI:3550066	cd8.
ACCESSION	AF015524		
VERSION	AF015524.1		
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	1 (bases 1 to 1546)		

AUTHORS TITLE	JOURNAL	REFERENCE	AUTHORS TITLE	JOURNAL	FEATURES
Gish, K., McClanahan, T. K. and Moore, K. W. A Novel Human Chemokine Receptor-Like Gene Expressed in Activated Monocytes Unpublished	2 (bases 1 to 1546)	Gish, K., McClanahan, T. K. and Moore, K. W. Direct Submission Submitted (22-JUL-1997) Molecular Biology, DNAX Research Institute, 901 California Avenue, Palo Alto, CA 94304, USA	Location/Qualifiers	1. .1546	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /chromosomes="3" /map="3p21.3" /cell_type="primary monocytes; activated"
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Matches 1035;	Conservative	0;	Mismatches	0;	Gaps 0;
Qy	1	ATGGCCAAATTACACGCTGGCACCAGAGGATGAATATGATGTCTCTCATAGAAGTGAACTG	60		
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Qy	61	GAGAGCGATGAGCGAGCAATGTGACAAAGTATGACGCCCGCAGGCACTCTCAGCCCCAGCTG	120		
Db	144	GAGAGCGATGAGCGAGCAATGTGACAAAGTATGACGCCCGCAGGCACTCTCAGCCCCAGCTG	203		
Qy	121	GTGCCATCATCTGCTCTGCTGTGTTTGTGATCGGTGTCTCTGGACAATCTCTCTGGTTGTG	180		
Db	204	GTGCCATCATCTGCTCTGCTGTGTTTGTGATCGGTGTCTCTGGACAATCTCTCTGGTTGTG	263		
Qy	181	CTTATCCTGGTAAAAATATAAGGACCTCAACCGGTGGAAAAATCTATCTCTTCAAACTTG	240		
Db	264	CTTATCCTGGTAAAAATATAAGGACCTCAACCGGTGGAAAAATCTATCTCTTCAAACTTG	323		
Qy	241	GCAGTTTCTAACTGTGTGTTTCTTGTTTACCCTGCCCTCTCTGGGCTCATGTGGGGGCGAT	300		
Db	324	GCAGTTTCTAACTGTGTGTTTCTTGTTTACCCTGCCCTCTCTGGGCTCATGTGGGGGCGAT	383		
Qy	301	CCCATGTGAAAAATCTCTCAATTTGGAAGTGTATCTTGTGGGCTGTACAGTGAGACATTTTTC	360		
Db	384	CCCATGTGAAAAATCTCTCAATTTGGAAGTGTATCTTGTGGGCTGTACAGTGAGACATTTTTC	443		
Qy	361	AATTGCTTCTGACTGTGCAAGGTACCTAGTGTGTTTTCACAGGGCACTTTTCTCA	420		
Db	444	AATTGCTTCTGACTGTGCAAGGTACCTAGTGTGTTTTCACAGGGCACTTTTCTCA	503		
Qy	421	GCACGAGGAGGGTGCCCTGTGTGGCATCATTTACAAGTGTCTTGGCATGGGTAAACAGGCATT	480		
Db	504	GCACGAGGAGGGTGCCCTGTGTGGCATCATTTACAAGTGTCTTGGCATGGGTAAACAGGCATT	563		
Qy	481	CTGGCCCACTTTCCTGAAATTCGTGGTTTATAACCTCAGATGGAGACACAGAAATACAAG	540		
Db	564	CTGGCCCACTTTCCTGAAATTCGTGGTTTATAACCTCAGATGGAGACACAGAAATACAAG	623		

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 1790)
TITLE Gish, K., McClanahan, T.K. and Moore, K.W.
JOURNAL CRAM: A Novel Human Chemokine Receptor-Like Gene Expressed in
REFERENCE Activated Monocytes
AUTHORS 2 (bases 1 to 1790)
TITLE Gish, K., McClanahan, T.K. and Moore, K.W.
JOURNAL Direct Submission
SUBMITTED (22-JUL-1997) Molecular Biology, DNAX Research Institute,
901 California Avenue, Palo Alto, CA 94304, USA
FEATURES Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 1035; DB 9; Length 1790;
Best Local Similarity 100.0%; Pred. No. 2.8e-284;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCCCAATTACAGCTGGCCACGAGGATGAATATGATCTCTCATAGAAAGTGAACTG 60
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QY 481 CTGGCCCACTTTGCTGAATTCGTGGTTTATATAAACTCTCAGATGGAAGACCAAGATAAAG 540

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DB 868 TGTGCATTTAGCAGAACTCCCTTCCCTGCGAGCTGTAGACATCTTGGAGCAATTTTCTG 927
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QY 841 AGTGTTCACATCACTAAACTCATTCGCCACCACTGCTGCTGCAATCAACCTCTCTCTGTAT 900
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DB 1348 TCCACCGAAGTGTA 1362

AX454430 1475 bp DNA linear PAT 06-JUL-2002
Sequence 15 from Patent WO0208284.
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AX454430.1 GI:21713839
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
Patent: WO 0208284-A 15 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
; Paoni, Nicholas P. (US) ; Stephan, Jean-Philippe P. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)
Location/Qualifiers
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RESULT 5
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN

Query Match 99.7%; Score 1031.8; DB 6; Length 1475;
Best Local Similarity 99.8%; Pred. No. 2.3e-283;
Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGCCAAATACAGCTGGCCACAGAGATGAATATATGATGCTCATAGAGGTGAACCTG 60
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Qy 481 CTGGCCACTTTGCGCTGAATTCGTGGTATTAACCTCAGATGGAAGACCAAGATACAG 540
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Db 989 ACCCCACTTTCAAGCCAGGGGAGCTGCTGCAAAAGGCACTCAGGGGAGAACCTTGACCAT 1048
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Db 1049 TCCACCGAAGTGTAA 1063

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LOCUS AX490908
DEFINITION Sequence 15 from Patent WO0200690.
ACCESSION AX490908
VERSION AX490908.1 GI:22323791
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Pooni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0200690-A 15 03-JAN-2002;
Genentech, Inc. (US)
FEATURES
source Location/Qualifiers
1. 1475
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ORIGIN

Query Match 99.7%; Score 1031.8; DB 6; Length 1475;
Best Local Similarity 99.8%; Pred. No. 2.3e-283;
Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 89 GAGAGCGATGAGGAGAGCAATGACAAAGTATGACGCCAGGCACTCTCAGCCAGCTG 148
Qy 121 GTGCGATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 149 GTGCGATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 208
Qy 181 CTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
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Qy 541 TGTGCATTTAGCAGACTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600

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Db	749	TTTGCCGTAATGGTAGTCTTCTCTGATGTGGGGCCCTACAAATATGATATTTTCTG	808
Qy	781	TCCACTTTTCAAAGAACACTTCTCCCTGAGTGACCTGCAAGAGCAGCTACAAATCTGGACAAA	840
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Qy	841	AGTGTTCACATCACTAAACTCATCGCCACCACTGCTGCAATCAACCTCTCCTGTAT	900
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VERSION	CQ714577.1 GI:42275434		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	1		
AUTHORS	Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.		
TITLE	Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof		
JOURNAL	Patent: WO 02068579-A 511 06-SEP-2002;		
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Best Local Similarity 99.84; Pred. No. 2.3e-283;			
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Db	262	GAGAGCGATGAGGAGAGCAATGTGCAAGTATGAGCCCGAGGCACTCTCAGCCCGAGCTG	321
Qy	121	GTGCCATCACTCTGCTCTGCTGTTTGTGATCGGTGCTCTGGACAAATCTCCTGGTTGTG	180

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Qy	181	CTTATCTCGGTAAATATAAAGACATCAAAACGCGTGGAAAAATATCTATCTTTAAACCTTG	240
Db	382	CTTATCTCGGTAAATATAAAGACATCAAAACGCGTGGAAAAATATCTATCTTTAAACCTTG	441
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Qy	301	CCCATGTGTAAATATCTCAATTGGACTGTACTTCTGCGGCTGTGACAGTGAACATTTTTC	360
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Qy	361	AATTGCTTCTGACTGTGCAAAAGGTACCTAGTGTGTTTGTGCAAAAGGCAACTTTTCTCA	420
Db	562	AATTGCTTCTGACTGTGCAAAAGGTACCTAGTGTGTTTGTGCAAAAGGCAACTTTTCTCA	621
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Db	802	ACTTTAAATGAAACATTTCCGTTCTTGTCTCCCTCCCTATTTATTTTACATTTCTCTAT	861
Qy	661	GTGCAATGAGAAAAACACTAAAGTTTCAGGAGCAGAGGTATAGCCCTTTTCAAGCTTGT	720
Db	862	GTGCAATGAGAAAAACACTAAAGTTTCAGGAGCAGAGGTATAGCCCTTTTCAAGCTTGT	921
Qy	721	TTTGGCGTAAATGGTAGTCTTCTCTGATGTGGCGCCCTACAAATATTTGCAATTTTCTG	780
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Qy	781	TCACATTTCAAAGAACACTTCTCCCTGAGTACTGCAAGAGCAGCTACAAATCTGGACAAA	840
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DEFINITION	Sequence 1 from Patent WO2004083232.		
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VERSION	CQ882060.1 GI:54034770		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1

AUTHORS

Pettipher, R.

TITLE

Receptor proteins

Patent: WO 2004083232-A 1 30-SEP-2004;

JOURNAL

Oxigen Limited (GB)

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Location/Qualifiers

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ORIGIN

Query Match 99.7%; Score 1031.8; DB 6; Length 1645;

Best Local Similarity 99.8%; Pred. No. 2.3e-283;

Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 61 GAGAGCGATGAGGAGGAGGATGACAGATGACAGCGCCAGGACCTCTCAGCCAGCTG 120
DB 263 GAGAGCGATGAGGAGGAGGATGACAGATGACAGCGCCAGGACCTCTCAGCCAGCTG 322
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LOCUS AX549068
DEFINITION Sequence 353 from Patent WO02061087.
ACCESSION AX549068
VERSION AX549068.1 GI:25813844
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Burmer, G.C., Roush, C.L. and Brown, J.P.
TITLE Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic peptides
JOURNAL Patent: WO 02061087-A 353 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
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Query Match 99.7%; Score 1031.8; DB 6; Length 1645;
Best Local Similarity 99.8%; Pred. No. 2.3e-283;
Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGGCCAAATTACAGCTGGCCACAGAGGATGAATATGATGTCCTCATAGAGGTGAACCTG 60
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DEFINITION Homo sapiens chemokine receptor X (CKRX) mRNA, complete cds.
ACCESSION AF014958
VERSION AF014958.1 GI:2305263
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1698)
AUTHORS Ansari-Lari,M.A., Liu,X.-M., Gorrell,J.H. and Gibbs,R.A.
TITLE Haplotype analysis of a gene cluster containing CCR5 and a new
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JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

member of chemokine receptor gene family
Unpublished
2 (bases 1 to 1698)
Ansari-Lari,M.A., Liu,X.-M., Gorrell,J.H. and Gibbs,R.A.
Direct Submission
Submitted (18-JUL-1997) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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ORIGIN

Query Match 99.7%; Score 1031.8; DB 9; Length 1698;
Best Local Similarity 99.8%; Pred. No. 2.3e-283; Indels 0; Gaps 0;
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RESULT 12	BC025717	1770 bp	mrna	linear	PRI 30-JUN-2004
LOCUS	Homo sapiens chemokine (C-C motif) receptor-like 2, mRNA (cdna				
DEFINITION	clone MGC:34104 IMAGE:5228561), complete cds.				
ACCESSION	BC025717				
VERSION	BC025717.1	GI:19343936			
KEYWORDS	MGC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

REFERENCE	1	(bases 1 to 1770)
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.	
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
PUBMED	12477932	
REFERENCE	2	(bases 1 to 1770)
AUTHORS	Strausberg, R.	
TITLE	Direct Submission	
JOURNAL	Submitted (06-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	

REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgabs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc.mgc@nih.gov Akher, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-I., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Madsen, O.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsougeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found


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RESULT 14

HSU95626

LOCUS

DEFINITION

HSU95626 Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6
143068 bp DNA linear PRI 16-MAY-1997

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ACCESSION U95626
VERSION 1
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 143068)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
2 (bases 1 to 143068)
AUTHORS McCombie, R.W., Wilson, R., Chen, E., Gibbs, R., Zuo, L., Johnson, D.,
Khan, M., Parnell, L., Dedhia, N., Ansari, A., Mardis, E., Schutz, K.,
Gnoj, L., de la Bastide, M., Kaplan, N., Greco, T., Touchman, J.,
Muzny, D., Chen, C.-N., Evans, C., FitzGerald, M., See, L.H., Tang, M.,
Porcel, B.M., Dragan, Y., Giacalone, J., Pae, A., Powell, E.,
Solinsky, K.A., Desilva, U., Diaz-Perez, S., Zhou, X., Yu, Y.,
Watanabe, M., Doggett, N., Garcia, D. and Sagripanti, J.-L.
Human BAC clone 110P12
Unpublished (1997)
2 (bases 1 to 143068)
AUTHORS McCombie, R.W., Wilson, R., Chen, E., Gibbs, R., Zuo, L., Johnson, D.,
Khan, M., Parnell, L., Dedhia, N., Ansari, A., Mardis, E., Schutz, K.,
Gnoj, L., de la Bastide, M., Kaplan, N., Greco, T., Touchman, J.,
Muzny, D., Chen, C.-N., Evans, C., FitzGerald, M., See, L.H., Tang, M.,
Porcel, B.M., Dragan, Y., Giacalone, J., Pae, A., Powell, E.,
Solinsky, K.A., Desilva, U., Diaz-Perez, S., Zhou, X., Yu, Y.,
Watanabe, M., Doggett, N., Garcia, D. and Sagripanti, J.-L.
Direct Submission
TITLE Submitted (27-MAR-1997) Advanced Genome Sequence Analysis Course,
JOURNAL Cold Spring Harbor Laboratory, 1Bungtown Rd., Cold Spring Harbor,
NY 11724, USA
COMMENT Regions with single-strand coverage are as follows:
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ORIGIN
Query Match 99.7%; Score 1031.8; DB 9; Length 143068;
Best Local Similarity 99.8%; Pred. No. 2.8e-283;
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Qy 421 GCCAGGAGGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db |||||
Qy 97062 GCCAGGAGGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 97121
Db |||||
Qy 481 CTGGCCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db |||||
Qy 97122 CTGGCCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 97181
Db |||||
Qy 541 TGTGCAATTTAGCAGAACTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
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Qy 97182 TGTGCAATTTAGCAGAACTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 97241
Db |||||

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QY 601 ACTTTAAATGACATTTTCGGTTCTTGCTCCCTCATTTATTTTACATTTCTCTAT 660
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Db 97362 TTTGGCGTAAATGATCTCTCTCTGATGTGGGCGCCCTACATATTCGATTTTTCCTG 97421
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QY 841 AGTGTTCACATCACTAAATCATCGCCACACCCACTGCTGCATCAACCCCTCTCTGTAT 900
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QY 1021 TCCACCGAAGTGTA 1035
Db 97662 TCCACCGAAGTGTA 97676

RESULT 15
AC098613
LOCUS Homo sapiens chromosome 3 clone RP11-24F11, complete sequence.
DEFINITION AC098613
AC098613
VERSION AC098613.2 GI:22038607
KEYWORDS HRG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 185437)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
and Haugen,E.D.
Direct Submission
Unpublished
2 (bases 1 to 185437)
AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
Direct Submission
TITLE Submitted (26-OCT-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
REFERENCE 3 (bases 1 to 185437)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
and Haugen,E.D.
Direct Submission
TITLE Submitted (01-AUG-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
COMMENT On Aug 1, 2002 this sequence version replaced gi:16445164.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Web site: <http://www.genome.washington.edu>
Contact: uwgctg@u.washington.edu
----- Project Information
Center project name: chr-3
Center clone name: RP11-24F11 (bc0137)
----- Summary Statistics
Sequencing vector: plasmid; L08752; 100% of reads

Chemistry: Dye-terminator ET; 93% of reads
Chemistry: Dye-terminator Big Dye; 7% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 184860 bases at least Q40
Consensus quality: 185398 bases at least Q30
Consensus quality: 185435 bases at least Q20
Insert size: 185437; sum-of-contigs
Quality coverage: 7.6x in Q20 bases; sum-of-contigs

Overlapping Sequences:
5': BAC-110P12 U95626, 111014-bp overlap
3': RP11-509121 (UMGC:bc0454) AC104304, 61294-bp overlap

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:
This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below.
The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC.
Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

BgIII				EcoRI				HindIII			
SeqDerMap	FngrPnt	SeqDerMap	FngrPnt	SeqDerMap	FngrPnt	SeqDerMap	FngrPnt	SeqDerMap	FngrPnt	SeqDerMap	FngrPnt
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2067	2065	-----	-----	1846	1824	3986	449	6501	<800	6501	10229
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5681	5720	-----	-----	4052	3986	1130	6592	10229	10229	10229	10229
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
3716	3953	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
875	897	-----	-----	1159	1130	6592	6501	6501	<800	6501	10229
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910	897	-----	-----	54	<800	10449	10229	10229	10229	10229	10229
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2169	2215	-----	-----	560	<800	3078	3985	3985	3985	3985	3985
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5763	5720	-----	-----	4905	4891	1054	1025	1025	1025	1025	1025
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5844	5720	-----	-----	3049	3078	3985	3985	3985	3985	3985	3985
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5061	5001	-----	-----	1377	1394	1100	1025	1025	1025	1025	1025
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9428	9684	1307	1304	11020	10820	Matches 1033; Conservative	0;	Mismatches 2; Indels 0; Gaps 0;
3809	3953	13306	13328	1978	1968			
1275	1234	2423	2450	8741	8681	Qy 1	ATGCCCAATTACACGCTGGCACCAGAGATGAATATGATGTCTCTCATAGAGGTGAACCTG	60
3351	3381	2243	2267	4795	4815	Db	ATGCCCAATTACACGCTGGCACCAGAGATGAATATGATGTCTCTCATAGAGGTGAACCTG	64668
193	<800	1109	1130	14921	14985	Qy	GAGAGCGATGAGGAGGAGCAATGTGCAAGTATGACGCCGCCAGGCACTCTCAGCCAGCTG	120
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9155	9107	332	<800	2091	2172	Db	GTGCCATCACTCTGCTCTGCTGTGTTGTGATCGGTGCTCTGGACAAATCTCTGGTTGTG	64788
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752	752	7881	7987	1565	1603	Db	CCCATGTGTAATAATCTCATTTGACCTGTACTCTTGGTGGCCCTGTACAGTGACACATTTTC	64968
1624	1653	7533	7635	1645	1603	Qy	AATTGCCCTCTGACTGTGCAAGGTACTAGTGTGTTTGGCAAGGGCAACTTTTCTCA	420
3258	3381	585	<800	573	<800	Db	AATTGCCCTCTGACTGTGCAAGGTACTAGTGTGTTTGGCAAGGGCAACTTTTCTCA	65028
9624	9684	2998	2973	7986	7830	Qy	GCCAGGAGGAGGTGCCCTGTGGCATCATTAAGTGTCTTGGCATGGGTAAACGCCATT	480
2841	2870	8796	8837	2313	2324	Db	GCCAGGAGGAGGTGCCCTGTGGCATCATTAAGTGTCTTGGCATGGGTAAACGCCATT	65088
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3898	3953	7102	7161	1250	1267	Db	CTGGCCATTTGGCTGAAATTCGTGGTTTATAAACCTCAGATGGAAGACCAGAAATACAG	65148
4830	4804			2290	2324	Qy	TGTGCATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACATCTCGAAGCAATTTCTG	600
2418	2459			2056	1968	Db	TGTGCATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACATCTCGAAGCAATTTCTG	65208
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Qy	841	AGTGTTCACATCACTAAACTCATCGCCACCA	CCCACTGTGCAATCAACCCCTCTCTGTAT	900
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Qy	961	ACCCCACTTCAACCCAGGGGGCAGTCTGCA	CAAGGCACATCGAGGGAAGAACCTGACCAT	1020
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Qy	1021	TCCACCGAAGTGTA	1035	
Db	65629	TCCACCGAAGTGTA	65643	

Search completed: June 18, 2005, 09:52:53
Job time : 4763.26 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 18, 2005, 06:35:24 ; Search time 4974.74 Seconds
(without alignments)
10548.684 Million cell updates/sec

Title: US-10-623-472-32
Perfect score: 1083
Sequence: 1 atggataactacacagtggc.....aaaggcaggataataataa 1083

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.on.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1083	100.0	1793	10	BC038631 Mus muscu
3	1083	100.0	1858	10	AB009384 Mus muscu
4	1081.4	99.9	1790	10	AF316576 Mus muscu
5	1081.4	99.9	163165	10	AC118727 Mus muscu
6	1081.4	99.9	230772	10	AC132832 Mus muscu
7	1076.6	99.4	1182	10	MMU318863 Mus muscu
8	1076.6	99.4	2045	6	AX454145 Sequence
9	1076.6	99.4	2045	10	AF030185 Mus muscu
10	840.2	77.6	231984	2	AC112401 Rattus no
11	428.6	39.6	1195	4	AB119274 Sus scrof
12	428.6	39.6	1314	4	AB119273 Sus scrof
13	428.6	39.6	144233	4	AP006435 Sus scrof
14	428.6	39.6	165558	4	AP006185 Sus scrof
15	423.6	39.1	1644	6	CO714577 Sequence
16	423.6	39.1	1755	9	BC071682 Homo sapi
17	423.6	39.1	185437	9	AC098613 Homo sapi
18	422	39.0	1475	6	AX454430 Sequence
19	422	39.0	1475	6	AX490908 Sequence

20	422	39.0	1645	6	CQ882060	Sequence
21	422	39.0	1645	6	AX549068	Sequence
22	422	39.0	1698	9	AF014958	Homo sapi
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27	420.4	38.8	1546	9	AF015524	Homo sapi
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33	412.4	38.1	1035	6	AX521743	Sequence
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37	236	21.8	588	6	AX079344	Sequence
38	218.8	20.2	7644	6	AX345787	Sequence
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ALIGNMENTS

RESULT 1
AX521744
LOCUS AX521744 1083 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 32 from Patent WO02057779.
ACCESSION AX521744
VERSION AX521744.1 GI:23572792
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
AUTHORS Boddeke, E.H. and Biber, K.
TITLE Cloning and expression of a new mcp receptor in glial cells
JOURNAL Patent: WO 02057779-A 32 25-JUL-2002;
Rijksuniversiteit Groningen (NL)
FEATURES
Location/Qualifiers
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misc_feature 1..1083
/note="mCCR12 chemokine receptor sequence"

ORIGIN

Query Match 100.0%; Score 1083; DB 6; Length 1083;
Best Local Similarity 100.0%; Pred. No. 5.4e-260;
Matches 1083; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 61 CTGGACAACAGTGGCCCGGACGATGTCCGCCCGGACGATGTCTTCCCCCAGCAGGTG 120
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Qy 181 ATCTTGTGGAATACAAAAGGACTCAAGAACTCTGGGGAACATCTACTTCTTAAACCTGGCA 240

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Qy	361	AGCAGGTGTTTTCCAAACATCTCTCTCTGTGTGCAAGATACAGGTTGTTTCCCAAGG	420	
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Qy	421	CGACTGGCCTCATCTTTCAGCACAGTGTCTTGTGCTATTTGTTCGTGCATCTCTGGCATGG	480	
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Db	601	AAGTACGTTCTGACGTCAAAATCATCATCTTTGTGCTTGTCTTCTCTGCTGCTGTTTTT	660	
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Db	1021	GAAGTCTATGGCAGGCCCATTTGAACCTGTACAGCAATTTGCAATCAAGGCAAGATATAA	1080	
Qy	1081	TAA 1083		
Db	1081	TAA 1083		

RESULT 2

BC038631

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

BC038631

Mus musculus chemokine (C-C motif) receptor-like 2, mRNA (cDNA clone MGC:47919 IMAGE:1347006), complete cds.

BC038631

BC038631.1

GI:24047248

Mus musculus (house mouse)

1793 bp

mRNA

linear

ROD 07-OCT-2003

ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 1793) Strausberg,R.L., Reingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shennan,C.M., Schuler,G.D., Altschul,S.F., Zerborg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Haieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Spapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toehiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullah,S.J., Bosak,S.A., McSwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J.J., Helton,E., Kettman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (36), 16899-16903 (2002)
MEDLINE	22388257
PUBMED	123477932
REFERENCE	2 (bases 1 to 1793) Strausberg,R.
AUTHORS	Direct Submission
TITLE	Submitted (15-OCT-2002) National Institutes of Health, Mammalian
JOURNAL	Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgapsb-rc@mail.nih.gov Tissue Procurement: Marcello Bento Soares, Ph.D. CDNA Library Preparation: M. Bento Soares, University of Iowa CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbio.org contact: anadan@systemsbiology.org Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAC Plate: 83 Row: b Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 8567367. Location/Qualifiers 1. .1793 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="MGC:47919 IMAGE:1347006" /tissue_type="Mammary gland" /clone_lib="Soares_mammary_gland_NbMWG" /lab_host="DH10B" /notes="Vector: pTT3-Pac" 1. .1793 /gene="Ccr12" /notes="synonyms: L-CCR, E01, CCR11" /db_xref="LocusID:54199" /db_xref="MGI:1920904" 178. .1260 /gene="Ccr12" /codon_start=1 /product="Ccr12 protein" /protein_id="AAH38631.1" /db_xref="GI:24047249"
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Qy 421 CGACTGGCCTCCATCTTCAACAGAGTGTCTTGTGGTATTTGTGCGTCATCTCGCAATGG 480  
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Db 958 GTGCTTTTCTGCTGCTTTCCAGGAACACTTGTCTCCTGCGAGGTGAGAGAGCAGCTAC 1017  
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AB009384 Mus musculus mRNA for L-CCR, complete cds. linear ROD 28-APR-1998  
LOCUS  
DEFINITION  
ACCESSION AB009384  
VERSION AB009384.1 GI:3090450  
KEYWORDS L-CCR.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (sites)  
REFERENCE  
AUTHORS Shimada,T., Matsumoto,M., Tatsumi,Y., Kanamaru,A. and Akira,S.  
TITLE A novel lipopolysaccharide inducible C-C chemokine receptor related  
gene in murine macrophages  
JOURNAL FEBS Lett. 425 (3), 490-494 (1998)  
MEDLINE 98222983  
PUBMED 9563519  
REFERENCE  
AUTHORS Akira,S. and Shimada,T.  
TITLE Direct Submission  
JOURNAL Submitted (02-DEC-1997) Shizuoka Akita, Hyogo College of Medicine,  
Department of Biochemistry; Mukogawa-cho 1-1, Nishinomiya, Hyogo  
663-8501, Japan (E-mail:akira@hyo-med.ac.jp, Tel:+81-798-45-6357,  
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DEFINITION	Mus musculus putative beta chemokine receptor (E01) mRNA, complete cds.				
ACCESSION	AF316576				
VERSION	AF316576.1 GI:11120630				
KEYWORDS					
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 1790)				
TITLE	Luo,Y., Berman,M.A., Fischer,F.R., Abromson-Leeman,S.R., Kuziel,W.A., Gerard,C. and Dorf,M.E.				
JOURNAL	RANTES and eotaxin stimulate chemotaxis, chemokine/cytokine synthesis, and receptor modulation in murine astrocytes				
REFERENCE	Unpublished				
AUTHORS	2 (bases 1 to 1790)				
TITLE	Berman,M.A. and Dorf,M.E.				
JOURNAL	Direct Submission				
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DEFINITION	Mus musculus chromosome 9, clone RP23-48D19, complete sequence.		
ACCESSION	AC132832		
VERSION	AC132832.13	GI:50540835	
KEYWORDS	HTG.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	1 (bases 1 to 230772)		
AUTHORS	Birren, B., Nusbaum, C. and Lander, E.		
TITLE	Mus musculus chromosome 9, clone RP23-48D19		

JOURNAL
REFERENCE
AUTHORS

Unpublished
2 (bases 1 to 230772)
Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Baetien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Gordon, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kelle, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rhee, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (04-SEP-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 230772)

JOURNAL
REFERENCE
AUTHORS

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Baetien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArrellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rhee, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (29-MAY-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 230772)

JOURNAL
REFERENCE
AUTHORS

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Baetien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArrellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rhee, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (23-JUL-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Db	210399	AGCAGGTGTTTCCAAATCCTCTCTGTGCAAGGATACAGGGTGTCTTTCCCAAGG	210458
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Qy	961	CCAGGTGCAATGATATCCCTATCAAGTAGTGGAGCTATCAGCAAGCCCTCCAAAG	1020
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Qy	1021	GAAGGTATGCGACGGCCATTGAATCTGTACAGCAATTTGATCAAGAGGAGATATAA	1080
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Db	211119	TAA 211121	
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DEFINITION	Mus musculus mRNA for putative G-protein coupled beta chemokine receptor (CCR11 gene).		
ACCESSION	AJ318863		
VERSION	AJ318863.1	GI:15886862	
KEYWORDS	CCR11 gene; G-protein coupled beta chemokine receptor.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	1 Biber, K.P.H. Cloning and characterisation of a new MCP-1 chemokine receptor CCR11		
AUTHORS	Zuurman, M.W.		
JOURNAL	Unpublished		
REFERENCE	2 LPS induced expression of a novel MCP chemokine receptor (CCR11) in mouse glial cells in vitro and in vivo		
AUTHORS	Unpublished		
TITLE			
JOURNAL			

REFERENCE	3 (bases 1 to 1182)	
AUTHORS	Biber, K.P.H.	
TITLE	Direct Submission	
JOURNAL	Submitted (09-AUG-2001) Biber K.P.H., Medical Physiology, State University Groningen, Ant. Deusinglaan 1, 9713 AV Groningen, NETHERLANDS	
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Qy	361	AGCGAGTGTGTTTCCAAACATCTCTCTTGTGTGCAAGGATACAGGGTGTGTTTCCCAAGG 420
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Qy	481	GCCATGGCTACTGGCTCTCTTTGCGCGGAGTCTGTGTTTATGAGCCTCGGATGGAAGA 540
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Qy	541	CAGAAACAAAGTGTGCTTTGGCAACCTCACCTTCTTGCCAACTCGAAGCGCGCTCTGG	600
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Db	719	ATAATCTGCTGACGGCAACTGAGGAGAAAGCAGAGCTTCAGGAGAGACAGTACGACCTC	778
Qy	721	CACAGCCCGCTCTTGTGCATAACGGCGGTGTTCTTTTGTGATGTGGGCGCCTTACACACT	780
Db	779	CACAGCCCGCTCTTGTGCATAACGGCGGTGTTCTTTTGTGATGTGGGCGCCTTACACACT	838
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Qy	841	CACCTGGACGCAAGTGTTCAGGTACACAGCTGGTAGCGACCAACCACCTGCTCGTCAAC	900
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Db	1139	TAA 1141	
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DEFINITION	Sequence 29 from Patent WO0203793.		
ACCESSION	AX454145		
VERSION	AX454145.1 GI:21713776		
KEYWORDS			
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	1		
AUTHORS	Allen, K.D. and Brennan, T.J.		
TITLE	Transgenic mice containing targeted gene disruptions		
JOURNAL	Patent: WO 0203793-A 29 17-JAN-2002;		
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Query Match	99.4%;	Score 1076.6; DB 6; Length 2045;	
Best Local Similarity	99.6%;	Pred. No. 2.2e-258;	
Matches 1079; Conservative	0; Mismatches 4; Indels 0; Gaps 0;		
Qy	1	ATGATTAACCTACAGTGGCGCCCGGACGATGAATATGATGCTCTTAATCTTAGACGACTAC	60
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Qy	121	CTGCAGTCTTCTGCTGCGCGGTGTTTGGGTGGGTCTCTTGGACAACGTTGCTGGCGGTGTTT	180
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Qy	781	GTGCTTTTCTGCTGCTCTTTCCAGGAACACTTGTCTCCCTGAGGATGAGAAAGACAGCTAC	840
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Qy	961	CCAGGTGCAATGATATCCCTATCAAGTAGTGGAGGCTTATCAGCAAGCGCTTCCAAAG	1020
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Db	1465	GAAGGTCAATGGAGGCCATTAAGTCTGATACAGCAATTTGATCAAGGAGAGATATAATA	1524
Qy	1081	TAA 1083	
Db	1525	TAA 1527	

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RESULT 9
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LOCUS
DEFINITION    Mus musculus putative beta chemokine receptor (E01) mRNA, complete
cds.
ACCESSION    AF030185
VERSION      AF030185.1  GI:2623640
KEYWORDS
SOURCE
ORGANISM      Mus musculus (house mouse)
REFERENCE
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL      Berman, M.A. and Dorf, M.E.
REFERENCE    1 (bases 1 to 2045)
AUTHORS      Mus. musculus E01 mRNA, complete cds
TITLE        Unpublished (1997)
JOURNAL
AUTHORS      Berman, M.A. and Dorf, M.E.
TITLE        Direct Submission
JOURNAL      Submitted (15-OCT-1997) Pathology, Harvard University Medical
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gene
CDS
Query Match      99.4%; Score 1076.6; DB 10; Length 2045;
Best Local Similarity 99.6%; Pred. No. 2.2e-258;
Matches 1079; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 ATGATAACTACACAGTGGCCCGGACGATGATATGATGTCCTTAATCTTAGACGACTAC 60
DB 445 ATGATAACTACACAGTGGCCCGGACGATGATATGATGTCCTTAATCTTAGACGACTAC 504
QY 61 CTGACAAACAGTGGCCCGGACCAAGTTCGGGCCCGGACGATGTCCTTCTCCCGCCGACGAGTG 120
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QY 121 CTCAGTTCCTGCTCGCGGTGTTTGGCGGTGCTCTTGACACACGTCGTCGGCGGTGTTT 180
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QY 1081 TAA 1083
DB 1525 TAA 1527

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RESULT 10

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AC112401/c
LOCUS
DEFINITION    Rattus norvegicus clone CH230-182H10, *** SEQUENCING IN PROGRESS
*** 3 unordered pieces.
AC112401
VERSION      AC112401.4  GI:23270069
KEYWORDS     HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM    Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 231984)
Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alebrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Bliswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, B.,

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Direct Submission
Unpublished
2 (bases 1 to 231984)
Worley,K.C.

Direct Submission
Submitted (21-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 231984)

Rat Genome Sequencing Consortium.
Direct Submission
Submitted (09-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 23, 2002 this sequence version replaced gi:21739980.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information

Center project name: GRU
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ACCESSION AP006185
VERSION AP006185.1 GI:41688294
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1
AUTHORS Shinkai,H., Morozumi,T., Toki,D., Muneta,Y., Awata,T. and Uenishi,H.
TITLE Cloning of porcine CC chemokine receptor genes and clustering structure on SSC13
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 165558)
AUTHORS Shinkai,H. and Uenishi,H.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-2003) Hiroki Shinkai, STAFF-Institute; 446-1 Ippaizuka, Kamiyokoba, Tsukuba, Ibaraki 305-0854, Japan (E-mail:sinkaie@gene.staff.or.jp, Tel:81-29-838-2190, Fax:81-29-838-2337)

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLES Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 511 06-SEP-2002;
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Db 1258 GA 1259

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Job time : 4979.74 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 18, 2005, 06:38:50 ; Search time 3956.26 Seconds
(without alignments)
9958.019 Million cell updates/sec

Title: US-10-623-472-31

Perfect score: 1035

Sequence: 1 atggcaattacacgtggc.....accattccaccgaagtgtaa 1035

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: gb_est1.*

2: gb_est2.*

3: gb_est3.*

4: gb_est4.*

5: gb_est5.*

6: gb_est6.*

7: gb_est7.*

8: gb_gse1.*

9: gb_gse2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	677	65.4	716	7	CF147784
3	637.8	61.6	729	6	CD370587
4	617.6	59.7	720	6	CD520843
5	609.8	58.9	831	4	B1834559
6	594.4	57.4	773	7	CO959196
7	526.6	50.9	880	4	B1819787
8	470.2	45.4	750	2	BE871331
9	440.4	42.6	768	6	CD468404
10	433	41.8	1035	4	EG386374
11	421.6	40.7	736	6	CD466140
12	414	40.0	2111	3	AK007808
13	397	38.4	789	6	CD466479
14	391.4	37.8	728	7	CO959203
15	389.4	37.6	683	6	CD535056
16	385.4	37.2	650	6	CD467795
17	384.8	37.2	664	6	CD470054
18	384.6	37.2	673	6	CD466424
19	383	37.0	691	6	CD468594
20	381.6	36.9	654	6	CD466568
21	368.2	35.6	623	6	CD471186
22	364	35.2	749	6	CD468632
23	363.4	35.1	724	6	CD469405
24	355.8	34.4	702	6	CD468196

ALIGNMENTS

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IMAGE:6192227 5', mRNA sequence.
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BQ892457
VERSION
BQ892457.1 GI:22284471
KEYWORDS
EST.
SOURCE
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ORGANISM
Homo sapiens
REFERENCE
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Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
NIH-MGC http://mgs.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL13593 row: 0 column: 12
High quality sequence stop: 601.
Location/Qualifiers
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/clone_lib="Lupski_sympathetic trunk"
/notes="Vector: pCMV-SORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCAGCGTCGCG-3' and 5'-GACTACTTCTAGTCGAGCGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life

25 353.8 34.2 692 7 CN786392
26 338 32.7 592 6 CD536762
27 335.4 32.4 793 6 CD466229
28 334.8 32.3 592 6 CD471634
29 331.4 32.0 578 6 CD465152
30 325 31.4 581 5 BP300486
31 319.4 30.9 576 5 BP295805
32 318 30.7 556 6 CD471194
33 316 30.5 885 4 B1082667
34 316 30.4 581 6 CD465288
35 313.2 30.3 564 6 CD472150
36 313 30.2 560 6 CD466412
37 311.4 30.1 561 6 CD464967
38 309.8 29.9 547 6 CD465726
39 299 28.9 581 5 BP300273
40 297.8 28.8 539 6 CD464212
41 296.2 28.6 542 6 CD469002
42 293 28.3 586 6 CD466472
43 293 28.3 618 6 CD467329
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DEFINITION			
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IMAGE:6971947 5', mRNA sequence.			
EST 25-JUL-2003			
716 bp mRNA linear			
CF147784			
LOCUS			
DEFINITION			
AGENCOURT 14740191 NIH MGC 145 Homo sapiens cDNA clone			
IMAGE:6971947 5', mRNA sequence.			
EST 25-JUL-2003			
716 bp mRNA linear			
CF147784			
LOCUS			
DEFINITION			
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IMAGE:6971947 5', mRNA sequence.			
EST 25-JUL-2003			
716 bp mRNA linear			
CF147784			
LOCUS			
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IMAGE:6971947 5', mRNA sequence.			
EST 25-JUL-2003			
716 bp mRNA linear			
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DEFINITION			
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EST 25-JUL-2003			
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ACCESSION
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VERSION
  CD370587.1 GI:31154677
KEYWORDS
  EST.
SOURCE
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  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 729)
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapb-remail.nih.gov
  Tissue Procurement: Dr. Gary W. Hunninghake, U of I
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  Cloning by: Dr. M. Bento Soares, University of Iowa
  Cloning Distribution: Distribution information can be found at
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FEATURES

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  NCI CGAP Ft1 is a normalized cDNA library constructed from
  a pool of 81 RNA samples from Alveolar Macrophages
  challenged with different treatments. The mRNA samples
  were a mixture of these conditions (times refer to
  incubations following isolation by bronchoalveolar lavage)
  (some normal donor macrophages were cultured in some of
  the conditions, other donor macrophages in different
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ORIGIN

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TAG TISSUE=Human Lung Alveolar Macrophage
TAG LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

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Qy      1031 TGTA 1035
Db       |||||
        71  TGTA 67

RESULT 4
CD520843
LOCUS   CD520843               720 bp    mRNA     linear    EST 06-JUN-2003
DEFINITION AGENCOURT 14369985 NIH MGC 191 Homo sapiens cDNA clone
IMAGE:30409698 5', mRNA sequence.
ACCESSION CD520843
VERSION   CD520843.1 GI:31452561
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 720)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Daniela S. Gerhard, Ph.D.
          Office of Cancer Genomics
          National Cancer Institute / NIH
          Bldg. 31 Rm10A07 Bethesda, MD 20892
          Email: cdapbs-x@mail.nih.gov
          Tissue Procurement: Narayan Bhat
          cDNA Library Preparation: CLONTECH Laboratories, Inc.
          DNA sequencing by: The I.M.A.G.E. Consortium (LLNL)
          Cloning strategy: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: NDCM198 row: k column: 19
          High quality sequence stop: 497.

FEATURES             source
                    1..720
                        Location/Qualifiers
                            /organism="Homo sapiens"
                            /mol_type="mRNA"
                            /db_xref="taxon:9606"
                            /clone="IMAGE:30409698"
                            /tissue_type="Pooled"
                            /lab_host="DH10B (TI phage-resistant)"
                            /clone_lib="NIH MGC 191"
                            /note="vector: pDNR-LIB; Site 1: SfII (ggccattatgcc);
                                Site 2: SfiI (ggcgcttgccc); Library is oligo-dT primed
                                and directionally cloned. PBMC - Peripheral Blood
                                Mononuclear Cells. RNA was pooled from 3/6hour stimulation
                                with PMA adn Ionomycin. 5' and 3' adaptors were used in
                                cloning as follows: 5' adaptor sequence:
                                5'-CAGCGCCATTATGCC-3', and 3' adaptor sequence:
                                5'-ATTCTAGAGGCGGGCGGCATG-T(30)BN-3', (where B = A,
                                C, or G and N = A, C, G, or T). Average insert size 1.69
                                kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
                                by PCR. This library was enriched for full-length clones
                                and was constructed by Clontech Laboratories (Palo Alto,
                                CA). Note: this is a NIH_MGC Library."

ORIGIN
Query Match           59.7%; Score 617.6; DB 6; Length 720;
Best Local Similarity 97.1%; Pred.No. 8.2e-169;
Matches 629; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy      1 ATGCCCAATTACAGCTGGCACAGAGTGAAATATGTCCTCATAGAGGTGAATG 60
Db      65 ATGCCCAATTACAGCTGGCACAGAGTGAAATATGTCCTCATAGAGGTGAATG 124
Qy      61 GAGAGCGATGAGGCAGACGAATGTGACAAGTATGACGCCAGGCACACTCTCAGCCCAGCTG 120
Db      125 GAGAGCGATGAGGCAGACGAATGTGACAAGTATGACGCCAGGCACACTCTCAGCCCAGCTG 184
Qy      121 GTGCCATCACTCTGCTGTGTGTGTGTGATCGGTGTCTCTGGACAATCTCTGGTTGTG 180

```


male. Library is oligo-dT primed and directionally cloned (ECORV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 58.9%; Score 609.8; DB 4; Length 831;
Best Local Similarity 99.4%; Pred. No. 1.6e-166;
Matches 633; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
Qy 1 ATGGCCATTACAGCTGGCCAGAGATGAATATGATGCTCTCATAGAGGTGAACCTG 60
Db 194 ATGGCCATTACAGCTGGCCAGAGATGAATATGATGCTCTCATAGAGGTGAACCTG 253
Qy 61 GAGAGCGATGAGGAGAGCAATGTGACAAATATGAGCCAGGCACTCTAGCCAGCTG 120
Db 254 GAGAGCGATGAGGAGAGCAATGTGACAAATATGAGCCAGGCACTCTAGCCAGCTG 313
Qy 121 GTGCATCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 314 GTGCATCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 373
Qy 181 CTATCTCTGTAATAATAAAGGACTCAACCGCTGGAAATATCTATCTCTAAACTTG 240
Db 374 CTATCTCTGTAATAATAAAGGACTCAACCGCTGGAAATATCTATCTCTAAACTTG 433
Qy 241 GCAGTTTCTAATGTTGTTCTTCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 434 GCAGTTTCTAATGTTGTTCTTCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTG 493
Qy 301 CCCATGTGTAATAATCTCATTTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 494 CCCATGTGTAATAATCTCATTTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 553
Qy 361 AATTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 554 AATTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 613
Qy 421 GCCAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 479
Db 614 GCCAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 673
Qy 480 TCTGCCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 538
Db 674 TCTGCCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 733
Qy 539 AGTGTGATTTAGCAGAACTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 598
Db 734 AGTGTGATTTAGCAGAACTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 793
Qy 599 TGACITTTAAATAATGAACATTTGGTTCTGCTGCTGCTGCTGCTGCTGCTGCT 635
Db 794 TGACITTTAAATAATGAACATTTGGTTCTGCTGCTGCTGCTGCTGCTGCTGCT 830

RESULT 6
CO959196/c
LOCUS
DEFINITION AGENCOURT 30842374 NIH MGC 146 Homo sapiens cDNA clone
IMAGE:7389718 3', mRNA sequence.
ACCESSION CO959196
VERSION CO959196.1 GI:51323776
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 773)
NIH-MGC <http://mgs.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL

COMMENT

Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: csapob-remail.nih.gov
Tissue Procurement: Guthrie cDNA Resource Center
cDNA Library Preparation: Guthrie cDNA Resource Center
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: IRB17 row: d column: 08
High quality sequence start: 18
High quality sequence stop: 630.

FEATURES

source

1..773
/organism="Homo sapiens"
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/clones="IMAGE:7389718"
/tissue_type="mixed"
/lab_host="DH10B (Ti-phage-resistant)"
/clone_lib="NIH_MGC_146"
/notes="vector: pCDNA3.1; Site 1: multiple; Site 2:
multiple; ORF's were PCR-amplified (from IMAGE clones or
from commercially available cDNA libraries) and cloned by
the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
into pCDNA3.1. For specific information on cloning sites
(which vary by clone), please refer to the Guthrie
website, using the Guthrie ID given in the file
[ftp://image.llnl.gov/image.rearrayed_plates/IRBF.presv.dat](http://image.llnl.gov/image.rearrayed_plates/IRBF.presv.dat)
a. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 57.4%; Score 594.4; DB 7; Length 773;
Best Local Similarity 98.2%; Pred. No. 5.1e-162;
Matches 610; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
Qy 414 TTTCTCAGCAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473
Db 638 TTTTTCAGCAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 579
Qy 474 AGCCATTTCTGCGCACTTTTGGCTGAAATTCGTGGTTTATAAACTCAGATGGAAGAC 533
Db 578 AGCCATTTCTGCGCACTTTTGGCTGAAATTCGTGGTTTATAAACTCAGATGGAAGAC 519
Qy 534 ATACAAGTGTGCAATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTTCTGGA 593
Db 518 ATACAAGTGTGCAATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTTCTGGA 459
Qy 594 TTTTCTGACITTTAAAAATGAACATTTTCGGTTCTTGTCTCTCCCTCTATTTTACAT 653
Db 458 TTTTCTGACITTTAAAAATGAACATTTTCGGTTCTTGTCTCTCCCTCTATTTTACAT 399
Qy 654 TCTCTATGTGCAATGAGAAAAACACTAAGGTTTCCAGGAGCAGAGGTATAGCTTTTCAA 713
Db 398 TCTCTATGTGCAATGAGAAAAACACTAAGGTTTCCAGGAGCAGAGGTATAGCTTTTCAA 339
Qy 714 GCTTGTGTTTGGCGTAATGTTAGTCTTCTCTGATGTGGCGGCTTACAATATTTGAT 773
Db 338 GCTTGTGTTTGGCGTAATGTTAGTCTTCTCTGATGTGGCGGCTTACAATATTTGAT 279
Qy 774 TTTTCTGCTGCACTTTCAAGAAACACTTTCTCCCTGAGTGACTGCAAGAGCAGCTACA 833
Db 278 TTTTCTGCTGCACTTTCAAGAAACACTTTCTCCCTGAGTGACTGCAAGAGCAGCTACA 219
Qy 834 GGACAAAGTGTTCACATCACTAACTCATCGCCACACCCACCTGCTGCTGCTGCTGCT 893
Db 218 GGACAAAGTGTTCACATCACTAACTCATCGCCACACCCACCTGCTGCTGCTGCTGCT 159
Qy 894 CTGTATGCGTTTCTTGTGAGGACATTTAGCAAAATACCTCTGCGCGCTGTTTCCATCT 953
Db 953 CTGTATGCGTTTCTTGTGAGGACATTTAGCAAAATACCTCTGCGCGCTGTTTCCATCT

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Db      158  CCTGTATCGCTTTCTTATGGGACATTTAGCAATACCTCTGCGCGTGTTCATCTGG 99
Qy      954  TAGTAACACCCCACTTCAACCCAGGGGCGAGTGTGCACAAGGCACATCGAGGGAAGACC 1013
Db      98   TAGTAACACCCCACTTCAACCCAGGGGCGAGTGTGCACAAGGCACATCGAGGGAAGACC 39
Qy      1014 TGACCAATTCACCGAAGTGTA 1034
Db      38   TGACCA-TCCACCGAAGTGTA 19

RESULT 7
BI819787
LOCUS   880 bp mRNA linear EST 04-OCT-2001
DEFINITION
603041489F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5182006 5',
mRNA sequence.
ACCESSION
BI819787
VERSION
BI819787.1 GI:15931337
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 880)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11454 Row: b Column: 23
High quality sequence stop: 809.
Location/Qualifiers
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/clone="IMAGE:5182006"
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/clone_lib="NIH_MGC_115"
/notes="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 50.9%; Score 526.6; DB 4; Length 880;
Best Local Similarity 93.9%; Pred. No. 3.6e-142;
Matches 604; Conservative 0; Mismatches 29; Indels 10; Gaps 5;

Qy      1 ATGCCCAATTACAGCTGGCAGACAGGATGATATGATCTCTCATAGAGTGAAGT 60
Db      239  ATGCCCAATTACAGCTGGCAGCAGAGGATGAATATGATCTCTCATAGAGTGAAGT 298
Qy      61   GAGAGCGATCAGGACGAATGTGACAACTATGACCCAGGCACCTCTCAGCCAGCTG 120
Db      299  GAGAGCGATGAGGAGGCAATGTGACAACTATGACCCAGGCACCTCTCAGCCAGCTG 358
Qy      121  GTGCCATCACTGCTGCTGTGTTTGTGATCGGTGTCGTGACAAATCTCTGTTGTG 180
Db      359  GTGCCATCACTGCTGCTGCTGTTGTGATCGGTGTCGTGACAAATCTCTGTTGTG 418
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Qy      181  CTTATCTCTGGTAAATATATAAGAGCTCAAAACGGTGGAAAATATCTATCTTAAACTTG 240
Db      419  CTTATCTCTGGTAAATATATAAGAGCTCAAAACGGTGGAAAATATCTATCTTAAACTTG 478
Qy      241  GCAGTTTCTAAACTTGTGTTTCTTGTCTTACCCTTGCCCTTCTGGGCTCATGCTGGGGGCGAT 300
Db      479  GCAGTTTCTAAACTTGTGTTTCTTGTCTTACCCTTGCCCTTCTGGGCTCATGCTGGGGGCGAT 538
Qy      301  CCCATGTGTAAATTTCTCATTTGAGACTGTACTTGTGGGCTGTACAGTGAGAGACATTTTTC 360
Db      539  CCCATGTGTAAATTTCTCATTTGAGACTGTACTTGTGGGCTGTACAGTGAGAGACATTTTTC 598
Qy      361  AATTGCTTCTGACTGTGCAAGGTACCTAGTGTGTTTTCACAAAGGCGCACTTTTCTCTCA 420
Db      599  AATTGCTTCTGACTGTGCAAGGTACCTAGTGTG-TATTGCAAGGGAACATTTTCTCTCA 657
Qy      421  GCCAGGAGGAGGTGCCCTGT-GGCATCATTAACAAGTGTCTGGCATGGTAAACAGCCAT 479
Db      658  GCCAGGAGGAGGTGCCCTGTGGCATCATTAACAAGTGTCTGGCATGGTAAACAGCCAT 717
Qy      480  TCTGGCCACTTTGCGCT--GAATTGCGGTTTATAAACTCAGAT--GGAAGACCAAGAAAT 535
Db      718  TCTGGCCACTTTGCGCTTGAATTGCGTGGTTTATAAACTCAGATTTGGCAAGACCAAGAAAT 777
Qy      536  ACAAGTGTGCATTTAGCAGAACTCCCTTCTGCCAGCTGATGA---GACATTTCTGGAAG 591
Db      778  ACAAGTGTGCATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGCACCATCTGGAAG 837
Qy      592  CATTTTCTGACTTTAAATAAGCAATTCGGTTCCTGCTCTCC 634
Db      838  CATTTTCTGACTTTAAATGAACATTTGCTACTGCTCTACC 880

RESULT 8
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LOCUS   750 bp mRNA linear EST 20-OCT-2000
DEFINITION
601449442F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853378 5',
mRNA sequence.
ACCESSION
BE871331
VERSION
BE871331.1 GI:10320107
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 750)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9577 Row: c Column: 11
High quality sequence stop: 735.
Location/Qualifiers
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/notes="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.8 kb. Library constructed by Life
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FEATURES
source

1..750
Location/Qualifiers

Technologies. "

Email: mmoratt@uga.edu

ORIGIN	Query Match	45.4%	Score 470.2	DB 2	Length 750
	Best Local Similarity	95.2%	Pred. No. 1e-125		
	Matches 517	Conservative 0	Mismatches 23	Indels 3	Gaps 3
Qy	1	ATGGCCAAATTACAGCTGGCACCCAGAGAGATGAATATGATGCTCTCATAGAGGTGAAC	60		
Db	211	ATGGCCAAATTACAGCTGGCACCCAGAGAGATGAATATGATGCTCTCATAGAGGTGAAC	270		
Qy	61	GAGAGCGATGAGGCGAGCAATGTGACAAAGTATGACGCCAGGCACTCTCAGCCCACTG	120		
Db	271	GAGAGCGATGAGGCGAGCAATGTGACAAAGTATGACGCCAGGCACTCTCAGCCCACTG	330		
Qy	121	GTGGCATCACTCTGCTCGCTGTGTGTGTGATCGGTGTCTTGGACAATCTCTCTGTTGTG	180		
Db	331	GTGGCATCACTCTGCTCGCTGTGTGTGTGATCGGTGTCTTGGACAATCTCTCTGTTGTG	389		
Qy	181	CTTATCTCGTAAAAATAAAAGGACTCAAAACGCGTGGAAAAATATCTATCTCTTAAACTG	240		
Db	390	CTTATCTCGTAAAAATAAAAGGACTCAAAACGCGTGGAAAAATATCTATCTCTTAAACTG	449		
Qy	241	GCAGTTCTTAACTTGTGTTTCTTGCTTACCCTGCCCCTTCTGGGCTCATGCTGGGGCGAT	300		
Db	450	GCAGTTCTTAACTTGTGTTTCTTGCTTACCCTGCCCCTTCTGGGCTCATGCTGGGGCGAT	509		
Qy	301	CCCATGTGTAATAATTCCTCATTTGGACTGTACCTTCTGGGGCTCTACAGTGAGACATTTTTC	360		
Db	510	CCCATGTGTAATAATTCCTCATTTGGACTGTACCTTCTGGGGCTCTACAGTGAGACATTTTTC	568		
Qy	361	AATTGCCCTCTGACTGTGCAAGGTACCTAGTGTGTTTTGACAAAGGCAACTTTTTCTCA	420		
Db	569	AATTGCCCTCTGACTGTGCAAGGTACCTAGTGTGTTTTGACAAAGGCAACTTTTTCTCA	627		
Qy	421	GCCAGGAGGAGGGTGCCTGTGGGATCATTTACAAGTGTCTTGGCATGGGTAAACGCCATT	480		
Db	628	GCCAGGAGGAGGGTGCCTGTGGGATCATTTACAAGTGTCTTGGCATGGGTAAACGCCAAGT	687		
Qy	481	CTGGCCACTTTGCTGAAATTCGTGTTTTATAAACCCTCAGATGGAGACACAGAAATACAA	540		
Db	688	CTGGCCACTTTGCTGAAATTCGTGTTTTATAAACCCTCAGATGGAGACACAGAAATACAA	747		
Qy	541	TGT 543			
Db	748	TGT 750			

RESULT 9	
CD468404	
LOCUS	
DEFINITION	768 bp mRNA linear EST 04-JUN-2003 LeukoS3_3 Fl1.b1_A025 Stimulated peripheral blood leukocytes S3 Equus caballus cDNA clone LeukoS3_3_Fl1_A025 3', mRNA sequence.
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	CD468404.1 GI:31389672 EST.
ORGANISM	Equus caballus (horse) Equus caballus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE	
AUTHORS	Vandenplas M., Cordonnier-Pratt M.-M., Suzuki Y., Sugano S., Moore J.N., Liang C., Sun F., Sullivan R., Shah M. and Pratt, L.H.
TITLE	An EST database from equine (Equus caballus) stimulated peripheral blood leukocytes
JOURNAL	Unpublished (2003)
COMMENT	Other ESTs: LeukoS3_3 Fl1.g1_A025 Contact: Cordonnier-Pratt MM Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 Fax: 706 583 0210

Email: mmpratt@cuga.edu

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; tissue and RNA were prepared in the Department of Large Animal Medicine, University of Georgia; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.

Seq primer: Sug3 (CGACCTTCGAGCTCGAGCACA)

FEATURES

Location/Qualifiers
1..768
organism="Equus caballus"
mol_type="rRNA"
strain="Tennessee walking horse"
db_xref="taxon:9796"
clone="LeukoS3_3_F11_A025"
sex="female"
tissue_type="blood"
cell_type="leukocytes"
lab_host="DH10B-T1 phage-competent cells"
clone_lib="STIMulated phage library"
note="organ: circulatory system"
Site 1: XhoI; Site 2: XhoI;
polyA+ RNA from equine peripheral blood mononuclear cells isolated from a healthy adult horse, incubated for 4 hr with 10⁶ double-stranded cDNA was cloned into pTZ19. The resulting different DraIII sites of the cDNA library are as follows: DraIII site is CACTGTGG, 3' end of the cDNA is CACATGTC, 3' end of the cDNA is CACATGTC.

ORIGIN

Query Match	42.6%	Score 440.4	DB 6	Length 768
Best Local Similarity	76.9%	Pred. No. 5.4e-117		
Matches 569	Conservative 0	Mismatches 156	Indels 15	Gaps 2
Qy	296	GGGATCCCATGTGTAAAAATTCATTCGACTGTACCTTCGTGGGCGCTGTACAGTCGAGACAT	355	
Db	1	GGACCCCCAAGTGTCAAAATTCGGTAGCGCTCTCCTCTGTAGGCGCTATACAGTAGGCGAT	60	
Qy	356	TTTTTCAATTGCCCTTCCTGACTGTGCAAAAGGTACCTAGTGTGTTTTTTCACAAAGGCGCAACTTTT	415	
Db	61	TTTTTCAATGCCCTTCCTGACTGTGCAAAAGGTGCGCTGGTGTGTTTTTGTGACATGGAGACGCTTT	120	
Qy	416	TCTCAGCCAGGAGGAGGGTGCCCTGTGGCATCAATTAACAAGTGTCTCTGGCATGGGTACAG	475	
Db	121	CTCTC-----GGTGGCCCGTGGCATCATCAACAGTGTCTGGCATGGGGAATAG	168	
Qy	476	CGATTCTGGCCACTTTTGGCCGTGAATTCGTGTGTTTATAACCTTCAGATCGGAAGACCAGAAAT	535	
Db	169	CTATTCTGGTCTCTTTGGCCGTGAATGGTGTGTTTACGAACCCACAGGTGGAAAGCCAGAAAT	228	
Qy	536	ACAAGTGTGCATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACATTTCTGGAAGCATT	595	
Db	229	ATPAGTGTCTTTTGGCAACCTCATTTCTCTCGGCTGATGAGACGTTCTGGAAGCATT	288	
Qy	596	TCTGTACTTTAAATAATGAACTTTTCGGTCTTGTCCTCCCGCTATTATATTTTATCAATTC	655	
Db	289	TTCTGACCTTGAGGACGAACATTTTGTGGACTTCTTTTCCCACTGTGTTTTTATATATTT	348	
Qy	656	TCATGTGCAATGAGAAAACACTAAGTTCAGGGAGCAGAGGTATAGCCTTTTCAAGC	715	
Db	349	GCATGTGGCAATGAGAAAACAAATAAGATTTGGGAAAAGGAGATATGATCTTTTCAAGC	408	
Qy	716	TTGTTTTTCCCGTAATGGTAGTCTTCCTTCTGATGTGGGCGCCCTACAATATTGCAATTTT	775	
Db	409	TTGTTTTTCCCGTAATGGTTGTTTCTCTGATGTGGGACCCCTACAATGTTGCACTTT	468	
Qy	776	TCTGTGCCACTTTCAAAGAACACTTCTCCTGTAGTGACTGCAAGAGCAGCTACAAATCTGG	835	
Db	469	GCATTATCCACTTTCAAAGACTACTTCTGCTGCAAGATTCGAGCAGACTACAACTGG	528	


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/clone="Leukon2_2_B11_A024"
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/tissue_type="blood"
/cell_type="leukocytes"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Unstimulated peripheral blood leukocytes N2"
/note="Organ: circulatory system; Vector: pME18S-FL3;
Site 1: XhoI; Site 2: XhoI; The library was prepared from
polyA+ RNA from unstimulated equine peripheral blood
leukocytes isolated from a healthy adult horse.
Double-stranded cDNA was cloned unidirectionally into
different DraIII sites of the pME18S-FL3 vector (5-prime
DraIII site is CACTGTGTG, 3-prime DraIII site is
CACCATGTG). XhoI excises the cDNA insert."
```

ORIGIN

Query Match 40.7%; Score 421.6; DB 6; Length 736;
Best Local Similarity 77.4%; Pred. No. 3.7e-111;
Matches 543; Conservative 0; Mismatches 144; Indels 15; Gaps 2;

Qy 334 GTGGGCGCTGTACAGTGAGACATTTTCAATTGCGCTTCTGACTGTGCAAGGTACCTAGTG 393
Db 1 GTAGGCGCTATACAGTGAGGCGATTTTCAATGCCCTTCTGACTGTGCAAGGTGCTGTG 60

Qy 394 TTTTGGCAAGGGGCAACTTTTTCAGCCAGGAGGCGGCTGCTGGCATCATTAACA 453
Db 61 TTTTGTGATGAGAGCGCTTTTCCTC-----GGTGCCCGGTGGCATCATCA 108

Qy 454 AGTGCTCGGATGGGTACAGCCATTTCTGCCACTTTGCTGTAATCGTGGTTATATAA 513
Db 109 AGTGCTCGGATGGGGAATAGCTATTCTGTCTCTTTGCTGGAATGGTGTTTTACGA 168

Qy 514 CCTCAGATGGAAGACACAGAAATACAAGGTGCTATTAGCAGACTCCCTCTGCGAGCT 573
Db 169 CCACAGGTGGAAGCCAGAAATATAAGTCTCTTTGGCAACCTCATTTCTGCCGCT 228

Qy 574 GATGAGACATTTCTGGAAGCATTTTCTGACTTTTAAAAATGAACATTTGCGTTCTTCTC 633
Db 229 GATGAGACGTTCTGGAAGCATTTTCTGACTTTGAGGAGCAACATTTTGGAGCTTCTTT 288

Qy 634 CCCCTATTATTATTACATTTCTCTATGTGCAGATGAGAAAACACTTAAGGTTGAGGAG 693
Db 289 CCACGTGTTGTTTATATTGCTATGTGCAATGAGAAAACAAATGAAGATTTGGGAAA 348

Qy 694 CAGAGGTATAGCTTTTCAAGCTTGTTTTGGCGTAATGTTAGTCTTCTCTCATGTGG 753
Db 349 AGGAGATATGATCTTTACAGCTTGTTTTGGCGTAATGTTTCTTCTCATGTGG 408

Qy 754 GCGCGCTACAAATATGCAATTTTCTGTCCACTTTTCAAGAACACTTCTCCCTGAGTGAC 813
Db 409 GGACCCCTAGCATGTTGCACTTTGCTTATCCACTTTCAAAGACTACTTCTGCTGCAAGAT 468

Qy 814 TGCAGAGCAGCAGTACATCTGACAAAAGTGTTCACATCACTAACTCATGCCACACACC 873
Db 469 TGCAGGCACAGCTCAACCTGACAAAAGTGTTCACATCATGAAATCGTCGCCACACACC 528

Qy 874 CACTGCTGATCAACCCCTCTCTGTATGCGTTTCTTGATGGGACATTTAGCAAAATACCTC 933
Db 529 CACTGCTGTCTCAACCGCTCTCTGATGCTTTCTTGCAAGGAATTTAGGAACACCTC 588

Qy 934 TGCGCGCTGTTTCCATCTCGGTAGTAAACCCCACTTCAACCCAGGGGCGAGTCTGCACAA 993
Db 589 TGCGCGCTTGCGCCATCTG---GGTAACGCTCCACCGCAACCCACTGAGAGATGCGCACCA 645

Qy 994 GGCAATCGAGGGGAAGAACCTGACCATCTCAACCCGAAGTGA 1035
Db 646 CGTACACGGGGGAAGAACACGACCTTTCTGCTGAAATGCAA 687

RESULT 12

AK007808

LOCUS

2111 bp mRNA linear HTC 03-APR-2004

DEFINITION

Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810047105 product:chemokine (C-C) receptor 1, -like 2, full insert sequence.

ACCESSION

AK007808.1 GI:12841594

VERSION

HTC; CAP trapper.

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 Carninci, P. and Hayashizaki, Y.

AUTHORS

High-efficiency full-length cDNA cloning

JOURNAL

Meth. Enzymol. 303, 19-44 (1999)

MEDLINE

99279253

PUBMED

10349636

REFERENCES

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

AUTHORS

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

TITLE

Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL

20499374

MEDLINE

11042159

PUBMED

11042159

REFERENCE

3 Shibata, K., Itoh, M., Aizawa, K., Nagao, K., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsu, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, Y., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuda, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

AUTHORS

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

TITLE

Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL

20530913

MEDLINE

11076861

PUBMED

11076861

REFERENCE

4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

AUTHORS

Functional annotation of a full-length mouse cDNA collection

TITLE

Nature 409, 685-690 (2001)

JOURNAL

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

AUTHORS

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

TITLE

Nature 420, 563-573 (2002)

JOURNAL

6 (bases 1 to 2111)

MEDLINE

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, P., Tanaka, T., Tejima, Y., Toyota, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

AUTHORS

Direct Submission

TITLE

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp)

JOURNAL

URL: http://genome.gsc.riken.jp/

Tel: 81-45-503-9222, Fax: 81-45-503-9216

COMMENT

Please visit our web site (<http://genome.gsc.riken.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken

Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; tissue and RNA were prepared in the Department of Large Animal Medicine, University of Georgia; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
Seq primer: Sug5 (CTTCTGCTCTAAAGCTGG).

FEATURES
source

Location/Qualifiers
1..789
/organism="Equus caballus"
/mol_type="mRNA"
/strain="thoroughbred"
/db_xref="taxon:9796"
/clones="Leukon2_4_E11_A024"
/sex="male"
/tissue_type="blood"
/cell_type="leukocytes"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Unstimulated peripheral blood leukocytes N2"
/note="Organ: circulatory system; Vector: pME18S-FL3;
Site1: XhoI; Site2: XhoI; The library was prepared from polyA+ RNA from unstimulated equine peripheral blood leukocytes isolated from a healthy adult horse.
Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGTC, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

ORIGIN

Query Match 38.4%; Score 397; DB 6; Length 789;
Best Local Similarity 76.1%; Pred. No. 2.7e-104;
Matches 555; Conservative 0; Mismatches 140; Indels 34; Gaps 4;

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Db |||||
Qy 77 ATGGCTAATACAGCTCCACACGAGAGATGAATATGATGTCCTCATAGAGGAGCTG 136
Db |||||
Qy 61 GAGAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
Db |||||
Qy 137 AATA---ACAAGATAGAACAAATGCGACCAATATGACACCAAGATTCCTCAGCCAGCTG 193
Db |||||
Qy 121 GTGCCATCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db |||||
Qy 194 GTGCTGCTCTCTACAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 253
Db |||||
Qy 181 CTTATCCTGTAATAAATAAGGACTCAACGCTGGAAATATCTATCTTCTAAACCTG 240
Db |||||
Qy 254 CTTATCCTGTAATAAATAAGGACTCAACGCTGGAAATATCTATCTTCTAAACCTG 313
Qy |||||
Qy 241 GCAGTTTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 292
Db |||||
Qy 314 GCAGTTTCTAAATTTGTGTTTCTGCTTACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 373
Qy |||||
Qy 293 -----GGGCGCATCCCATGTAATAATTCATTTGACGTACTCTGCTGGGCTG 342
Db |||||
Qy 374 GGGGGGATTCGCGGAGCCCAAGTGTCAATTTCTGTAGGCTCTCTCTGTAGGCTA 433
Qy |||||
Qy 343 TACAGTGAGACATTTTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 402
Db |||||
Qy 434 TACAGTGAGGACATTTTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 493
Qy |||||
Qy 403 AAGGCAACATTTTCTCAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 462
Db |||||
Qy 494 ATGAGAGCGCTTTCCTC-----GGTGGCCGCTGGCATCATCAAGTGTCTG 541
Qy |||||
Qy 463 GCATGGGTAAACAGCATTTCGGCCACTTTGGCTCAATTTCTGCTGCTGCTGCTGCTGCTG 522
Db |||||
Qy 542 GCATGGGGAATAGCTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 601
Db |||||
Qy 523 GAAGACCAGAAATACAAAGTGTGCTTTAGCAGAACTCCCTTCTGCTGCTGCTGCTGCTG 582
Db |||||

Db |||||
Qy 583 TTCTGGAAGCATTTTCTGACCTTAAATGAACATTTGGTTCCTGCTGCTGCTGCTGCTGCT 642
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Qy 662 TTCTGGAAGCATTTTCTGACCTTAAATGAACATTTGGTTCCTGCTGCTGCTGCTGCTGCT 721
Qy 643 ATTTTACATTTCTCTATGTCGAATGAGAAAAACACATCAAGTTTCAGGAGCAGAGGTAT 702
Db |||||
Qy 722 GTTTTATATTTTGTCTATGTCGAATGAG-AAAACAATAAGATTTGGGAAAAGGAGATAT 780
Qy 703 AGCCTTTTC 711
Db |||||
Qy 781 GATCTTTTAC 789

RESULT 14
C0959203
LOCUS
DEFINITION
AGENCY 30842774 NIH MGC 146 Homo sapiens cDNA clone
IMAGE:7389718 5', mRNA sequence.
ACCESSION
C0959203
VERSION
C0959203.1 GI:51323783
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 728)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
CONTACT: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Guthrie cDNA Resource Center
cDNA Library Preparation: Guthrie cDNA Resource Center
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRB17 row: d column: 08
High quality sequence start: 68
High quality sequence stop: 638.
FEATURES
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/db_xref="taxon:9606"
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/tissue_type="mixed"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH MGC 146"
/notes="Vector: pCDNA3.1; Site 1: multiple; Site 2:
multiple; ORF's were PCR-amplified (from IMAGE clones or
from commercially available cDNA libraries) and cloned by
the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
into pCDNA3.1. For specific information on cloning sites
(which vary by clone), please refer to the Guthrie
website, using the Guthrie ID given in the file
ftp://image.llnl.gov/image_rearrayed_plates/IRBF.presv.dat
a. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 37.8%; Score 391.4; DB 7; Length 728;
Best Local Similarity 98.5%; Pred. No. 1.1e-102;
Matches 395; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGGCCAAATACAGCTGGCCACGAGAGATGAATATGATGTCCTCATAGAGGTGAACCTG 60
Db |||||

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Db      3  ATGGCCAATTACACGCTGGCACAGAGAAAGATATGATGTCCTCATAGAAAGTGAACTG 62
Qy      61  GAGAGCATTGAGGAGAGCAATGTGACAAGATGACGCCAGGCACTCTCAGCCAGCTG 120
Db      63  GAGAGCATTGAGGAGAGCAATGTGACAAGATGACGCCAGGCACTCTCAGCCAGCTG 122
Qy      121  GTGCATCACTCTGCTCTGCTGTGTTTGTGATCGGTCTCTGCGATCTGCGCAATCTCCTGTTGTG 180
Db      123  GTGCATCACTCTGCTCTGCTGTGTTTGTGATCGGTCTCTGCGATCTGCGCAATCTCCTGTTGTG 182
Qy      181  CTTATCTCTGTAATAATAAGGACTCAAAAGCGGTGGAATAATCTATCTTTAAACTTG 240
Db      183  CTTATCTCTGTAATAATAAGGACTCAAAAGCGGTGGAATAATCTATCTTTAAACTTG 242
Qy      241  GCAGTTTCTAACCTGTGTTTCTGCTTACCTGCGCTTCTGGGCTCATGCTGGGGGGAT 300
Db      243  GCAGTTTCTAACCTGTGTTTCTGCTTACCTGCGCTTCTGGGCTCATGCTGGGGGGAT 302
Qy      301  CCATGTGTAAATTCATTGGAAGTCTACTTCTGTTGGGCTGTACAGTGTAGACATTTTC 360
Db      303  CCATGTGTAAATTCATTGGAAGTCTACTTCTGTTGGGCTGTACAGTGTAGACATTTTC 362
Qy      361  AATTGCTCTTGAAGTGTGCAAGGTAACCTAGTGTGTTTGTCA 401
Db      363  AATTGCTCTTGAAGTGTGCAAGGTAACCTAGTGTGTTTGTCA 403
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RESULT 15

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LOCUS          Leukon5_3_C06.bi_A027 Unstimulated peripheral blood leukocytes N5
DEFINITION     Equus caballus cDNA clone Leukon5_3_C06_A027 3', mRNA sequence.
ACCESSION      CD535056
VERSION         CD535056.1 GI:31577471
KEYWORDS        EST.
SOURCE          Equus caballus (horse)
ORGANISM        Equus caballus
REFERENCE       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS         Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
1 (bases 1 to 683)
Vandenplas,M., Cordonnier-Pratt,M.-M., Suzuki,Y., Sugano,S.,
Moore,J.N., Liang,C., Sun,F., Sullivan,R., Shah,M. and Pratt,L.H.
An EST database from equine (Equus caballus) unstimulated
peripheral blood leukocytes
Unpublished (2003)
Other_ESTs: Leukon5_3_C06.g1_A027
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
```

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; tissue and RNA were prepared in the Department of Large Animal Medicine, University of Georgia; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA. Seq primer: Sug3 (CGACCTGCAGCTCGAGCACA)

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PolyA=Yes.
Location/Qualifiers
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/clone="Leukon5_3_C06_A027"
/sex="male"
/tissue_type="blood"
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FEATURES

source

Search completed: June 18, 2005, 12:07:55
Job time : 3963.26 secs

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/clone_lib="Unstimulated peripheral blood leukocytes N5"
/notes="Organ: circulatory system; Vector: pME18S-FL3,
Site 1: XhoI; Site 2: XhoI; The library was prepared from
polyA+ RNA from unstimulated equine peripheral blood
leukocytes isolated from a healthy adult horse.
Double-stranded cDNA was cloned unidirectionally into
different DraIII sites of the pME18S-FL3 vector (5-prime
DraIII site is CACGTGTG, 3-prime DraIII site is
CACCATGTG). XhoI excises the cDNA insert."
```

ORIGIN

```
Query Match      37.6%; Score 389.4; DB 6; Length 683;
Best Local Similarity 76.5%; Pred. No. 4.2e-102;
Matches 509; Conservative 0; Mismatches 141; Indels 15; Gaps 2;

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Qy      431  GGGTGCCTCTGGGCATCATTAAGA GTGCTCTGGCATGGGTAAAGCCATTCGGCCACTT 490
Db      50    -GGTGCCTCTGGGCATCATTAAGA GTGCTCTGGCATGGGTAAAGCCATTCGGCTCTCT 108
Qy      491  TGCCTGAA TTTGCTGTGTTTATAAAACCTCAGATGGAAGACCAGAAATACAAAGTGTGCAATTA 550
Db      109  TGCCTGAA TTTGCTGTGTTTATAGAACCAACAGTGGAAAGCCAGAAATATAGTGTCTTTG 168
Qy      551  GCAGAACTCCCTTCCTGGCAGCTGATGAGACATTTGGAAGCATTTTCTGACTTTTAAAAA 610
Db      169  GCAAACCTCATTTCTCTCGCGGTGATGAGACGTTCTGGAAGCATTTTCTGACCTTGAGGA 228
Qy      611  TGAACATTTTGGTCTTGTGCTCCCTCATTTATTTTACATTTCTCTATGTGCAATGA 670
Db      229  CGAACATTTTGGACTTCTTTTCCCACTGTTTGTATATCTTTGCTATGTGCGAATGA 288
Qy      671  GAAACACATAAGTTTCAGGAGCAGAGGTATAGCCTTTTCAAGCTTGTTTTGGCGTAA 730
Db      289  GAAACACATAAGTTTGGAAAGAGATATGATCTTTTCAAGCTTGTTTTGGCGTAA 348
Qy      731  TGGTAGTCTTCTCTTGTATGTGGGGCCCTACAATATTCATTTTCTGTCACATTTCA 790
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Qy      791  AAGAACATTTCTCCCTGAGTGTGCTCAAGAGCAGCTACAATCTGGACAAAGTGTTCACA 850
Db      409  AAGACTACTTCTGCTGCAAGACTTGAGGACAGCTACAACCTGGACAAAGTGTTCACA 468
Qy      851  TCACTAAACTCATGCGCACCCACTGCTGCATCAACCTCTCTCTGTATGGCTTTCTTG 910
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Qy      911  ATGGGACATTTAGCAAAATACCTCTGCGGTGTTTCCATCTGGGTAGTAAACCCCACTTC 970
Db      529  ACAAGGAATTTAGGAAACACTCTGCGGCTTTGGCCATCTG---GGTAACGGTCCACCGC 585
Qy      971  AACCCAGGGGCGAGTGTGCACAAGGCACATCGAGGGAAGAACTGACCATTCACCCGAG 1030
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Qy      1031  TGTAA 1035
Db      646  TGCNA 650
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
8515.071 Million cell updates/sec

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Perfect score: 1035

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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1035	100.0	1547	4	US-10-039-659A-11
2	1029.8	99.5	1270	4	US-08-016-434-756
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4	326.4	31.5	620	4	US-09-023-655-308
5	233	22.5	1059	3	US-09-517-605-8
6	233	22.5	1059	4	US-08-771-276-19
7	230.6	22.3	1059	3	US-08-724-984A-3
8	230.6	22.3	1225	4	US-09-023-655-967
9	230.6	22.3	1376	3	US-09-087-232A-12
10	230.6	22.3	1376	4	US-09-016-434-1104
11	230.6	22.3	1376	4	US-09-796-202-2
12	230.6	22.3	1414	4	US-09-502-783A-1
13	230.6	22.3	1414	4	US-09-502-784A-1
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17	230.6	22.3	1477	4	US-09-938-719-2
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19	230.6	22.3	3383	3	US-08-861-105-13
20	230.6	22.3	3383	3	US-08-575-967A-1
21	230.6	22.3	3383	4	US-09-023-655-951
22	230.6	22.3	3383	4	US-08-771-276-1
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24	229	22.1	1059	4	US-09-826-509-476
25	229	22.1	1071	3	US-09-087-232A-14
26	225.8	21.8	1414	3	US-08-466-343D-1
27	196.6	19.0	1065	3	US-08-847-296B-2

28 196.6 19.0 1139 4 US-08-375-199B-3 Sequence 3, Appli
29 196.6 19.0 1193 4 US-08-720-565-3 Sequence 3, Appli
30 196.6 19.0 1201 4 US-09-016-434-1085 Sequence 1085, Ap
31 196.6 19.0 1201 4 US-09-023-655-905 Sequence 905, App
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33 196.6 19.0 1915 3 US-08-575-967A-3 Sequence 3, Appli
34 196.6 19.0 1915 4 US-08-771-276-3 Sequence 3, Appli
35 194 18.7 2440 3 US-08-724-984A-1 Sequence 1, Appli
36 193.4 18.7 1068 4 US-09-826-509-474 Sequence 474, App
37 193.4 18.7 1689 4 US-08-720-565-1 Sequence 1, Appli
38 193.4 18.7 1689 4 US-09-931-381A-15 Sequence 15, Appli
39 193.4 18.7 1689 4 US-08-375-199B-1 Sequence 1, Appli
40 192.6 18.6 1116 4 US-08-720-565-5 Sequence 5, Appli
41 192.6 18.6 1116 4 US-08-375-199B-5 Sequence 5, Appli
42 189.8 18.3 1495 4 US-09-016-434-1190 Sequence 1190, Ap
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44 189.8 18.3 2156 1 US-08-012-988A-1 Sequence 1, Appli
45 189.8 18.3 2156 4 US-09-023-655-1247 Sequence 1247, Ap

ALIGNMENTS

RESULT 1

US-10-039-659A-11

; Sequence 11, Application US/10039659A

; Patent No. 6723520

; GENERAL INFORMATION:

; APPLICANT: Wang, Wei

; APPLICANT: Gish, Kurt C.

; APPLICANT: Schall, Thomas J.

; APPLICANT: Vicari, Alain P.

; APPLICANT: Zlotnik, Albert

; TITLE OF INVENTION: Antibodies that bind chemokine TECK

; FILE REFERENCE: DX0589K1B US

; CURRENT APPLICATION NUMBER: US/10/039,659A

; CURRENT FILING DATE: 2002-01-03

; PRIOR APPLICATION NUMBER: US 08/887,977

; PRIOR FILING DATE: 1997-07-03

; PRIOR APPLICATION NUMBER: US 60/021,664

; PRIOR FILING DATE: 1996-07-05

; PRIOR APPLICATION NUMBER: US 60/028,329

; PRIOR FILING DATE: 1996-10-11

; PRIOR APPLICATION NUMBER: US 60/048,593

; PRIOR FILING DATE: 1997-06-04

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 11

; LENGTH: 1547

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (49)..(1116)

; OTHER INFORMATION:

US-10-039-659A-11

Query Match 100.0%; Score 1035; DB 4; Length 1547;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCCCAATTACAGCTGGCACCAGGAGGATGAATATATGATGTCCTCATAGAGGTGAAGCTG 60

85 ATGCCCAATTACAGCTGGCACCAGGAGGATGAATATATGATGTCCTCATAGAGGTGAAGCTG 144

Qy 61 GAGAGCGATGAGGAGGAGCAATGTGACAACTATGACCCAGGCACTCTCAGCCAGCTG 120

145 GAGAGCGATGAGGAGGAGCAATGTGACAACTATGACCCAGGCACTCTCAGCCAGCTG 204

Qy 121 GTCCCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180

205 GTCCCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 264

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QY 181 CTTATCTCTGTAATAAATATAAGGACTCAAAACGGCTGGAAATATCTATCTTCTAAACTTG 240
DB |||||
DB 265 CTTATCTCTGTAATAAATATAAGGACTCAAAACGGCTGGAAATATCTATCTTCTAAACTTG 324
QY 241 GCAGTTTCTAACTTGTTTCTTGCTTAACCTGCCCTTCTGGGCTCATGCTGGGGCGAT 300
DB |||||
DB 325 GCAGTTTCTAACTTGTTTCTTGCTTAACCTGCCCTTCTGGGCTCATGCTGGGGCGAT 384
QY 301 CCCATGTGTAATAATCTCATGAGACTGTACTTGTGGGCTGTACAGTGAGACATTTTTC 360
DB |||||
DB 385 CCCATGTGTAATAATCTCATGAGACTGTACTTGTGGGCTGTACAGTGAGACATTTTTC 444
QY 361 AATTGGCTTCTGACTGTGCAAGGTACTAGTGTGTTTGGCAAGGCACTTTTCTCA 420
DB |||||
DB 445 AATTGGCTTCTGACTGTGCAAGGTACTAGTGTGTTTGGCAAGGCACTTTTCTCA 504
QY 421 GCCAGGAGGAGGTGCCCTGTGGCATCATTAACAAGTGTCTGGCATGGGTAACAGCCATT 480
DB |||||
DB 505 GCCAGGAGGAGGTGCCCTGTGGCATCATTAACAAGTGTCTGGCATGGGTAACAGCCATT 564
QY 481 CTGGCCACTTTGCTGTAATTCGTGGTTTATAAACCCTCAGATGGAAGCAGAAATACAG 540
DB |||||
DB 565 CTGGCCACTTTGCTGTAATTCGTGGTTTATAAACCCTCAGATGGAAGCAGAAATACAG 624
QY 541 TGTGCATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTCGGAAGCAATTTCTG 600
DB |||||
DB 625 TGTGCATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTCGGAAGCAATTTCTG 684
QY 601 ACTTTAAAAATGAACATTTCCGTTCTTGTCTCCCTCATTTATTTTACATTTCTAT 660
DB |||||
DB 685 ACTTTAAAAATGAACATTTCCGTTCTTGTCTCCCTCATTTATTTTACATTTCTAT 744
QY 661 GTGCAATGAGAAACACATAAGGTTTCCAGGAGCAGAGGTATAGCCCTTTCAAGCTGTT 720
DB |||||
DB 745 GTGCAATGAGAAACACATAAGGTTTCCAGGAGCAGAGGTATAGCCCTTTTCAAGCTGTT 804
QY 721 TTTGCCGTAATGTAGTCTTCTTCTGATGTGGCGCCCTTACAAATATTGCAATTTTCCCTG 780
DB |||||
DB 805 TTTGCCGTAATGTAGTCTTCTTCTGATGTGGCGCCCTTACAAATATTGCAATTTTCCCTG 864
QY 781 TCCACTTTTCAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTACAATCTGGACAA 840
DB |||||
DB 865 TCCACTTTTCAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTACAATCTGGACAA 924
QY 841 AGTGTTCACATCACTAAACTCATGCCACCACTGCTGCAATCAACCTCTCCTGAT 900
DB |||||
DB 925 AGTGTTCACATCACTAAACTCATGCCACCACTGCTGCAATCAACCTCTCCTGAT 984
QY 901 CGGTTTCTTGATGGGACATTTAGCAATACCTCTGCCGCTGTTTCCATCTGCGTAGTAAC 960
DB |||||
DB 985 CGGTTTCTTGATGGGACATTTAGCAATACCTCTGCCGCTGTTTCCATCTGCGTAGTAAC 1044
QY 961 ACCCCACTTCAACCCAGGGGCGAGTGTGCAAAAGGCACTGAGGGAAGAACTTGACCAT 1020
DB |||||
DB 1045 ACCCCACTTCAACCCAGGGGCGAGTGTGCAAAAGGCACTGAGGGAAGAACTTGACCAT 1104
QY 1021 TCCACCGAAGTGTA 1035
DB |||||
DB 1105 TCCACCGAAGTGTA 1119
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RESULT 2

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US-09-016-434-756
; Sequence 756, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
```

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STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 756:
SEQUENCE CHARACTERISTICS:
LENGTH: 1270 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: MPHGNOT03
CLONE: 442279
US-09-016-434-756
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Query Match 99.5%; Score 1029.8; DB 4; Length 1270;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1031; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGCCAAATTACACGCTGGCACACAGAGGATGAATATGATGTCTCTCATAGAGGTGAACCTG 60
DB 180 ATGGCCAAATTACACGCTGGCACACAGAGGATGAATATGATGTCTCTCATAGAGGTGAACCTG 239
QY 61 GAGAGCGATGAGCGAGAGCAATGTGACAAAGTATGACGCCAGGACCTCTCAGCCAGCTG 120
DB 240 GAGAGCGATGAGCGAGAGCAATGTGACAAAGTATGACGCCAGGACCTCTCAGCCAGCTG 239
QY 121 GTGCCATCACTCTGCTCTGCTGTGTTGTGATCGGTGTCTCTGGACAAATCTCTGTTGTG 180
DB 300 GTGCCATCACTCTGCTCTGCTGTGTTGTGATCGGTGTCTCTGGACAAATCTCTGTTGTG 359
QY 181 CTTATCTCGTGAATAATATAAGGACTCAAAACGGCTGGAAATATCTATCTTCTAAACTTG 240
DB 360 CTTATCTCGTGAATAATATAAGGACTCAAAACGGCTGGAAATATCTATCTTCTAAACTTG 419
QY 241 GCAGTTTCTAACTTGTTTCTTGCTTACCCTTCTGGCTCATGCTGGGGCGAT 300
DB 420 GCAGTTTCTAACTTGTTTCTTGCTTACCCTTCTGGCTCATGCTGGGGCGAT 479
QY 301 CCCATGTGTAATAATCTCATGAGACTGTACTTGTGGGCTGTACAGTGAGACATTTTTC 360
DB 480 CCCATGTGTAATAATCTCATGAGACTGTACTTGTGGGCTGTACAGTGAGACATTTTTC 539
QY 361 AATTGGCTTCTGACTGTGCAAGGTACTAGTGTGTTTGGCAAGGCACTTTTCTCA 420
DB 540 AATTGGCTTCTGACTGTGCAAGGTACTAGTGTGTTTGGCAAGGCACTTTTCTCA 599
QY 421 GCCAGGAGGAGGTGCCCTGTGGCATCATTAACAAGTGTCTGGCATGGGTAACAGCCATT 480
DB 600 GCCAGGAGGAGGTGCCCTGTGGCATCATTAACAAGTGTCTGGCATGGGTAACAGCCATT 659
QY 481 CTGGCCACTTTGCTGTAATTCGTGGTTTATAAACCCTCAGATGGAAGCAGAAATACAG 540
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Db 660 CTGCCACTTTGGCTGAAATAGTGGTTTATAAACCCTCAGATGGAAGACCAAGAAATACAAG 719
Qy 541 TGTGCATTTAGCAGAACTCCCTTCTGTCAGCTGATGAGACATTTCTGGAAGCAATTTTCTG 600
Db 720 TGTGCATTTAGCAGAACTCCCTTCTGTCAGCTGATGAGACATTTCTGGAAGCAATTTTCTG 779
Qy 601 ACTTTAAATAGAACTTTGGTTCTGTCCTCCCTTATTTATTTTACATTTCTCTAT 660
Db 780 ACTTTAAATAGAACTTTGGTTCTGTCCTCCCTTATTTATTTTACATTTCTCTAT 839
Qy 661 GTGCAATAGAAACAACTAAAGTTTCAAGGAGCAGAGGTATAGCTTTTCAAGCTTGT 720
Db 840 GTGCAATAGAAACAACTAAAGTTTCAAGGAGCAGAGGTATAGCTTTTCAAGCTTGT 899
Qy 721 TTTGCCGTAATGTTAGTCTTCTCTGATGAGGCGCCCTACAATATTTGCAATTTTCTG 780
Db 900 TTTGCCCAATAGTTAGTCTTCTCTGATGAGGCGCCCTACAATATTTGCAATTTTCTG 959
Qy 781 TCCATTTTCAAGAACTTCTCCTGAGTGACTGCAAGAGCAGCTACAATCTGGACAAA 840
Db 960 TCCATTTTCAAGAACTTCTCCTGAGTGACTGCAAGAGCAGCTACAATCTGGACAAA 1019
Qy 841 AGTGTTCACATCACTAACTCATCGCCACCACTGCTGCTGATCAACCTCTCTCTAT 900
Db 1020 AGTGTTCACATCACTAACTCATCGCCACCACTGCTGCTGATCAACCTCTCTCTAT 1079
Qy 901 GCGTTTCTGATGGGACATTTAGCAATACCTCTGCGCTGTTTCCATCTGCGTAGTAAC 960
Db 1080 GCGTTTCTGATGGGACATTTAGCAATACCTCTGCGCTGTTTCCATCTGCGTAGTAAC 1139
Qy 961 ACCCACTTCAACCCAGGGGAGTCTGCAAGGACATCGAGGGAAGAACTTGACCAT 1020
Db 1140 ACCCACTTCAACCCAGGGGAGTCTGCAAGGACATCGAGGGAAGAACTTGACCAT 1199
Qy 1021 TCCACCGAAGGTAA 1035
Db 1200 TCCACCGAAGGTAA 1214

RESULT 3

US-08-681-192-1
; Sequence 1, Application US/08681192
; Patent No. 6287801
; GENERAL INFORMATION:
; APPLICANT: BERGSM, DERK
; APPLICANT: ELSHOURBAGY, NABIL
; APPLICANT: SARAU, HENRY
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR HNF0578
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/681,192
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777

; REFERENCE/DOCKET NUMBER: ATG50014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5031
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1050 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; US-08-681-192-1

Query Match 94.0%; Score 973.4; DB 3; Length 1050;
Best Local Similarity 99.9%; Pred. No. 1.3e-309;
Matches 974; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGCCCAATTTACAGCTGGCACCAGAGGATGAATATGATGCTCATAGAAGGTGAACCTG 60
Db 76 ATGCCCAATTTACAGCTGGCACCAGAGGATGAATATGATGCTCATAGAAGGTGAACCTG 135
Qy 61 GAGAGCGATGAGGAGCAGCAATGTGCAAGTATGACGCCAGGCACTCTCAGCCCAAGCTG 120
Db 136 GAGAGCGATGAGGAGCAGCAATGTGCAAGTATGACGCCAGGCACTCTCAGCCCAAGCTG 195
Qy 121 GTGCCATCACTCTGCTGCTGCTGTTGTGATCGGTGCTCTGGACATCTCTCGTGTGTG 180
Db 196 GTGCCATCACTCTGCTGCTGTTGTGATCGGTGCTCTGGACATCTCTCGTGTGTG 255
Qy 181 CTTATCTCTGTAATAATAAAGGACTCAACCGGTGGAATAATCTATCTTCTAAACTTG 240
Db 256 CTTATCTCTGTAATAATAAAGGACTCAACCGGTGGAATAATCTATCTTCTAAACTTG 315
Qy 241 GCAGTTTCTAACTTGTGTTCTTGTCTTACCCTGCTTCTGGGCTCATGTGGGGGGCAT 300
Db 316 GCAGTTTCTAACTTGTGTTCTTGTCTTACCCTGCTTCTGGGCTCATGTGGGGGGCAT 375
Qy 301 CCATGTGTAATAATTCATCTGACCTGTACTTGTGGGCTGTACAGTGAGACATTTTTC 360
Db 376 CCATGTGTAATAATTCATCTGACCTGTACTTGTGGGCTGTACAGTGAGACATTTTTC 435
Qy 361 AATTGCTCTGACTGTGCAAGGTAAGTACTAGTGTGTTTGGACAGGCACTTTTCTCA 420
Db 436 AATTGCTCTGACTGTGCAAGGTAAGTACTAGTGTGTTTGGACAGGCACTTTTCTCA 495
Qy 421 GCCAGGAGGAGGTGCCCTGTGGCATCATTTACAAGTGTCTGGCATGGTAACAGCCATT 480
Db 496 GCCAGGAGGAGGTGCCCTGTGGCATCATTTACAAGTGTCTGGCATGGTAACAGCCATT 555
Qy 481 CTGGCACTTTGCTGCTGAATTCGTGGTTTATAAACCCTCAGATGGAAGACCAAGATACAAG 540
Db 556 CTGGCACTTTGCTGCTGAATTCGTGGTTTATAAACCCTCAGATGGAAGACCAAGATACAAG 615
Qy 541 TGTGCATTTTAGCAGAACTCCCTTCTGCGGCTTCTGCTCCCTATTTTATTTTACATTTTCTG 600
Db 616 TGTGCATTTTAGCAGAACTCCCTTCTGCGGCTTCTGCGGCTTCTGCGGCTTCTGCTG 675
Qy 601 ACTTTAAATAGAACTTTGCTGCTTCTGCTCCCTATTTTATTTTACATTTTCTCTAT 660
Db 676 ACTTTAAATAGAACTTTGCTGCTTCTGCTCCCTATTTTATTTTACATTTTCTCTAT 735
Qy 661 GTCAAAATGAGAAAAACACATAAGTTTCAAGGAGCAGAGGTATAGCCCTTTTCAAGCTGTT 720
Db 736 GTCAAAATGAGAAAAACACATAAGTTTCAAGGAGCAGAGGTATAGCCCTTTTCAAGCTGTT 795
Qy 721 TTTGCGGTAAATGCTAGTCTCTCTGATGAGGCGCCCTACATATTTGCAATTTTCTG 780
Db 796 TTTGCGGTAAATGCTAGTCTCTCTGATGAGGCGCCCTACATATTTGCAATTTTCTG 855

QY 781 TCCACTTTCAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTACAAATCTGGACAA 840
Db 856 TCCACTTTCAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTACAAATCTGGACAA 915
QY 841 AGTGTTTCAACATCACTAAACTCATCGCCACCAACCACCTGCTGCATCAACCCCTCTCCCTGAT 900
Db 916 AGTGTTTCAACATCACTAAACTCATCGCCACCAACCACCTGCTGCATCAACCCCTCTCCCTGAT 975
QY 901 GCGTTTCTGATGGGACATTTAGCAAAATACCTCTGCGCGTGTTCATCTGCGTAGTAAC 960
Db 976 GCGTTTCTGATGGGACATTTAGCAAAATACCTCTGCGCGTGTTCATCTGCGTAGTAAC 1035
QY 961 ACCCACTTCAACCC 975
Db 1036 ACCCACTTCAACCC 1050
RESULT 4
US-09-023-655-308
; Sequence 308, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Sellhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 308:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 620 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGNOT10
; CLONE: 1378524
; US-09-023-655-308
Query Match 31.5%; Score 326.4; DB 4; Length 620;
Best Local Similarity 99.7%; Pred. No. 1.1e-96;
Matches 327; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 708 TTTCAAGCTGTTTTCGCGTAATGGTAGTCTTCTCTCATGTGGGCGCCCTACAATAT 767
|||||

Db 5 TTTCAAGCTGTTTTCGCGTAATGGTAGTCTTCTCTCATGTGGGCGCCCTACAATAT 64
QY 768 TGCATTTTTCCTGTCACATTTCAAGAACACATTTCTCCCTGAGTGACTGCAAGAGCAGCTA 827
Db 65 TGCATTTTTCCTGTCACATTTCAAGAACACATTTCTCCCTGAGTGACTGCAAGAGCAGCTA 124
QY 828 CAATCTGGACAAAGTGTTCACATCACTAAACTCATCGCCACCAACCACCTGCTGCATCAA 887
Db 125 CAATCTGGACAAAGTGTTCACATCACTAAACTCATCGCCACCAACCACCTGCTGCATCAA 184
QY 888 CCCTCTCTCTGTATGCGTTTCTTGATGGGACATTTAGCAAAATACCTCTGCGCTGTTTCCA 947
Db 185 CCCTCTCTCTGTATGCGTTTCTTGATGGGACATTTAGCAAAATACCTCTGCGCTGTTTCCA 244
QY 948 TCTGCGTAGTAACACCCCACTTCAACCCAGGGGGCAGTCTGCACAAAGGCACATCGAGGGA 1007
Db 245 TCTGCGTAGTAACACCCCACTTCAACCCAGGGGGCAGTCTGCACAAAGGCACATCGAGGGA 304
QY 1008 AGAACCTGACCATTTCCACCAGTGTAA 1035
Db 305 AGAACCTGACCATTTCCACCAGTGTAA 332
RESULT 5
US-09-517-605-8
; Sequence 8, Application US/09517605
; Patent No. 6391567
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Kwon, Douglas S.
; APPLICANT: van Kooyk, Yvette
; APPLICANT: Geijtenbeck, Tneo
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/09/517,605
; CURRENT FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-517-605-8

Query Match 22.5%; Score 233; DB 3; Length 1059;
Best Local Similarity 56.8%; Pred. No. 9.6e-66;
Matches 531; Conservative 0; Mismatches 365; Indels 39; Gaps 4;
QY 54 TGAACCTGGAGAGCGATGAGCGAGCAATGTGACAAAGTATGAGCCCGAGCAGCTCTCAGC 113
Db 30 TGACATCGATTATGATACATCGGAGCCCTGCCAAAAAATCAATGTGAAGCAATCGAGC 89
QY 114 CCAGCTGGTGCCATCACTCTGCTCTGCTGTTTGTGATCGGTGTCTCTGGACAATCTCCT 173
Db 90 CCGCCTCTCTGCGCTCCACTCTACTCACTGGTGTTCATCTTTGGTTTGTGGCAACATGCT 149
QY 174 GGTGTGCTTATCCTGGTAAATATAAAGGACTCAAAACGGGTGGAAAAATATCTATCTTCT 233
Db 150 GGTCACTCTCGTCTGATAAACTGCAAAAGGCTGAAGAGCATGACATCTACCTGCT 209
QY 234 AACTTGGCAGTTCCTAACTTGTTTCTTGTCTTACCTCGCCCTCTGGCTCA----- 287
Db 210 CAACTGGGCGCATCTCGACTGTTTCTCTTCTTACTGTCCCCCTCTGGGCTCACTACGC 269
QY 288 -----TGCTGGGCGGATCCCATGTGTAAAAATTTCTCATTTGGACTGTACTCGT 335
Db 270 TGTGCCCCAGTGGGACTTTTGGAAAATACAAATGTGCAACTTTGACAGGGCTCTATTAT 329
QY 336 GGGCCTGTACAGTGAGACATTTTTCATTTGCTTCTGACTGTGCAAGGATACCTAGTGT 395
Db 330 AGGCTCTTCTCTGGAATCTTCTTCACTCATCTCTCTGCAAAATCGATAGATACCTAGCTAT 389
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396 TTTGCACAGGGCAACTTTTCTCAGCCAGGAGGGTGCCTGTGGCATCATTAAG 455
Db CGTCCATGCTGTGTTGCTTTTAAAGCC---AGGACGGTCACTTTGGGGTAGTGAAG 446
456 TGTCTGGCATGGGTAAACAGCAATCTTGGCCACTTTGGCTGAATTCGTGGTTTATAAACC 515
Db TGTGATCACTTGGGTGGTGTGTTGCTCTCCAGGAATCATCTTTACCATC 506
456 TCAGATGGAGACAGAAATACAAAGTGTGCAATTTAGCAAACTCCCTTCTGCGAGCTGA 575
Db TCAAAAGAGAGGCTTCTCATACACT- - - - -GCAGCTCTCATTTTCCATACAGTCA 557
576 TGAGACATCTCGAGCAATTTCTGACTTTTAAATGAACATTTGGTCTTCTGCTCC 635
Db GTATCAATTTCTGGAGAAATTTCCAGACATTAAGATAGTATCTTTGGGGTGGTCTGCTGCC 617
636 CCTATTATTTTACATTTCTCTATGTGCAATGAGAAACACTAA- - - - -GGTT 686
Db CTGCTTGTGATGCTCATCTGCTACTCGGAATCTTAAACACTGCTTGGTGTGCAAA 677
687 CAGGAGCAGAGGTATAGCCCTTTTCAAGCTTTGTTTGGCGTAAATGGTAGTCTTCTTCT 746
Db CGAGAGAGAGGACAGGCTGTGAGGCTTATCTTCAACCATCATGATTTGTTATTTCT 737
747 GATGTGGGCGCCCTACAAATATGCAATTTTCTGTCACATTTTCAAGAACACTTCTCCCT 806
Db CTTCTGGGCTCCCTACAAATTTGCTTCTCTGAAACACCTTCCAGGAATTTCTTTGGCCT 797
807 GAGTGACTGCAAGAGCAGCTACATCTGGCAAAAGTGTTCACATCACTAACTCATCGC 866
Db GAATAATGTCAGTGTCTTAACAGTTGGACCAAGCCATGAGGTGACAGAGCTCTTGG 857
867 CACCACCCTGCTGTCATCAACCTCTCTGATGCGTTTCTTGGTGGGACATTTAGCAA 926
Db GATGAGGCACTGCTGTCATCAACCCCATCATGCTTGTGTTGGGAGAGTTTCAAAA 917
927 ATACCTTGGCGCTGTTTCACTGCTGCTAGTAA 961
Db CTACCTTGTAGTCTTCTTCCAAAAGCATATTGCA 952

RESULT 6

US-08-771-276-19
; Sequence 19, Application US/08771276
; Patent No. 6797811
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicky L.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/771,276
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6797811and, Greta B.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1059 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1056
US-08-771-276-19

Query Match

Best Local Similarity 22.5%; Score 233; DB 4; Length 1059;
Pred. No. 9.6e-66;
Matches 531; Conservative 0; Mismatches 365; Indels 39; Gaps 4;

Qy 54 TGAACCTGAGAGCGATGAGCGAGCAATGTGACAGTATGACGCCAGGCACTCTCAGC 113
Db 30 TGACATCGATTATTATACATCGGAACCCCTGCCAAAATCAATGTGAACAAATCGCAGC 89
Qy 114 CCAGCTGGTGGCCATCACTCTGCTCTGCTGTGTTGTGATCGGTGCTCCTGGACAATCTCCT 173
Db 90 CCAGCTGGTGGCCCTGCTCTGCTCTGCTGTGTTGTGATCGGTGCTCCTGGACAATCTCCT 149
Qy 174 GGTGTGCTTATCCTGGTAAAAATATAAAGGACTCAAAAGCGGTGGAATATCTATCTCT 233
Db 150 GGTGTGCTTATCCTGGTAAAAATATAAAGGACTCAAAAGCGGTGGAATATCTATCTCT 209
Qy 234 AAACCTGGGAGTTTCTTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 292
Db 210 AAACCTGGGAGTTTCTTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 269
Qy 293 - - - - -GGGGCGATCCCATGTGTAAATTTCTCATTTGGAGCTGTACTTCTGT 335
Db 270 TGCTGCCAGTGGAGCTTTGGAAATACATGTGCTCAACTCTTGACAGGGCTCTATTATAT 329
Qy 336 GGGCTGTACAGTGAGACATTTTTCATATGCTCTTCTGACTGTGCAAAAGGTACCTAGTGT 395
Db 330 AGGCTTCTCTGGAATCTTCTTCAATCATCTCTGCAATCGATAGGTACCTGGCTAT 389
Qy 396 TTTGCACAGGGCACTTTTCTCAGCCAGGAGGGTGCCTGTGGCATCATTAAG 455
Db 390 CGTCCATGCTGTGTTGCTTTTAAAGCC---AGGACAGTCACTTTGGGGTGGTGAAG 446
Qy 456 TGTCTGGCATGGTAAACAGCAATCTGCGCACTTTTGGCTGAATTCGTGGTTTATAAACC 515
Db 447 TGTGATCACTTGGGTGGTGTGTTGCTCTCTCCAGGAATCATCTTTACCATC 506
Qy 516 TCAGATGGAGACAGAAATACAAAGTGTGCAATTTAGCAAACTCCCTTCTGCGAGCTGA 575
Db 507 TCAGAGAGAGGCTTCTCATTTACACT- - - - -GCAGCTCTCATTTTCCATACAGTCA 557
Qy 576 TGAGACATTTCTGGAAGCAATTTCTGACTTTTAAATGAACATTTGGTCTTCTGCTCC 635
Db 558 GTATCAATTTCTGGAAGAAATTTCCAGACATTAAGATAGTATCTTTGGGGTGGTCTGCTGCC 617
Qy 636 CCTATTATTTTACATTTCTCTATGTGCAATGAGAAACACTAA- - - - -GGTT 686
Db 618 GCTGCTTGTGATGCTCATCTGCTACTCGGAATCTTGAAGAACTCTGCTTGGTGTGCAAA 677
Qy 687 CAGGAGCAGAGGTATAGCCCTTTTCAAGCTTTGTTTGGCGTAAATGGTAGTCTTCTTCT 746
Db 678 CGAGAGAGAGGACAGGCTGTGAGGCTTATCTTCAACCATCATGATTTGTTATTTCT 737
Qy 747 GATGTGGGCGCCCTACAAATATGCAATTTTCTGTCACATTTTCAAGAACACTTCTCCT 806
Db 738 CTTGTGGGCTCCCTACAAATTTGCTTCTCTGAAACACCTTCCAGGAATTTCTTTGGCCT 797
Qy 807 GAGTGACTGCAAGAGCAGCTACATCTGGCAAAAGTGTTCACATCACTAACTCATCGC 866
Db 798 GAATAATGTCAGTGTCTTAACAGTTGGACCAAGCCATGAGGTGACAGAGCTCTTGG 857

Qy	867	CACACCCACTGCTGCATCAACCCCTCTCTGATATGCGTTTCTTATATGGACATTTAGCAA	922
Db	858	GATGACACACTGCTGCATCAACCCCATCATCTATGCTTTGTGCGGGAGAGTTTCAGAAA	917
Qy	927	ATACCTCTGCGCGCTGTTTCCCATCTGCGTAGTAACA	961
Db	918	CTACCTCTTACTCTTTCTTTCCAAAGCACATTGCCA	952
RESULT 7			
US-08-724-984A-3			
; Sequence 3, Application US/08724984A			
; Patent No. 638055			
; GENERAL INFORMATION:			
; APPLICANT: Derk Bergsma, Mary Brawner, and Usman Shabon			
; TITLE OF INVENTION: No. 6388055el Mouse Genomic Clone of the CC-			
; TITLE OF INVENTION: CXRS Receptor			
; NUMBER OF SEQUENCES: 5			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: SmithKline Beecham Corporation			
; STREET: 709 Swedeland Road, P.O. Box 1539			
; CITY: King of Prussia			
; STATE: PA			
; COUNTRY: USA			
; ZIP: 19406-0939			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE			
; COMPUTER: IBM 486			
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS			
; SOFTWARE: MICROSOFT WORD			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/724.984A			
; FILING DATE: October 3, 1996			
; CLASSIFICATION: 800			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER:			
; FILING DATE:			
; ATTORNEY/AGENT INFORMATION:			
; NAME: William T. Han			
; REGISTRATION NUMBER: 34,344			
; REFERENCE/DOCKET NUMBER: ATG50023			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 610 270 5024			
; TELEFAX: 610 270 5090			
; INFORMATION FOR SEQ ID NO: 3:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1059			
; TYPE: Nucleic Acid			
; STRANDEDNESS: Single			
; TOPOLOGY: Linear			
; ANTI-SENSE: No			
US-08-724-984A-3			
Query Match 22.3%; Score 230.6; DB 3; Length 1059;			
Best Local Similarity 57.0%; Pred. No. 6e-65;			
Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4			
Qy	74	CAGAGCAATGTGACAGTATGACGCCAGGCACTCTCAGCCAGCTGTGTGCCATCACTCT	133
Db	50	CGGAGCCCTGCCAAAAAATCAATGTGAAGCAATCGCAGCCCGCTCTCGCTCGCTCT	109
Qy	134	GCTCTGCTGTTTGTGATCGGTGTCCTGGACAAATCTCTCTGTTGTGCTTATCCTGGTAA	193
Db	110	ACTCACTGGTGTTCATCTTTGTTTGTGGGCAACATGCTGTGTCATCTTCATCCTGATAA	169
Qy	194	AATATAAAGGACTCAAAACGCGTGGAAAAATATCTATCTTCTAAACTTGGCAGTTTCTAACT	253
Db	170	ACTGCAAAAGGCTGAAGAGCATGACATGACATCTA	229
Qy	254	TGTGTTCTTGTGTTACCTGCGCTTCTGGGCTCATGCTGGGGGGG	298
Db	230	TGTTTTCTTCTTACTGTGCTTCTGGGCTCACTATGCTGCCGCCACAGTGGGACTTGTG	289

APPLICATION NUMBER: US/09/023.655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 967:
SEQUENCE CHARACTERISTICS:
LENGTH: 1225 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1502408
US-09-023-655-967

Query Match 22.3%; Score 230.6; DB 4; Length 1225;
Best Local Similarity 57.0%; Pred. No. 6.6e-65;
Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;

74 CAGAGCAATGTGACAAAGTATGACGCCAGGCACTCTCAGCCAGCTGGTGCATCACTCT 133
76 CGGAGCCCTGCCAAAATCAATGGAAGCAATGCGAGCCCGCTCTCGCTCGCTCT 135
134 GCTCGCTGCTTGTGATCGGTGCTCGGCAATCTCTGCTGTGTGCTTATCTCTGGTAA 193
136 ACTCACTGGTTCATCTTTGGTGTGCTGGCAACATGCTGTCTATCTCTGATAA 195
194 AATATAAGGACTCAACGGCTGGAAAATATCTATCTTCTAACTTGGCAGTCTTCACT 253
196 ACTGCAAAAGGCTGAAGAGCATGACTGACATCTACTGCTCAACCTGGCCATCTCTGACC 255
254 TGTGTTTCTGCTTACCTGCTGCTTCTGGGCTCATGCTGGGGGGG----- 298
256 TGTGTTTCTGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 315
299 ---ATCCCATGTGTAATAATCTCAATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCT 355
316 GAAATACAAATGTGCAACTCTTGACAGGCTCTATTTTATAGGCTTCTCTCTGGAATCT 375
356 TTTTCAATTTGCTTCTGCTGCAAGGTAACCTAGTGTGTTTTTGCACAAAGGCAACTTTT 415
376 TCTTCATCATCTCTCTGACAAATGATAGGTACCTGGCTGCTGCTCATGCTGTGTTGCTT 435
416 TCTCAGCAGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 475
436 TAAAGGCC---AGGACGGTCACTTTGGGGTGGTGACAAAGTGTGATCACTTTGGGTGGTG 492
476 CCATTTCTGGCCACTTTGCTGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 535
493 CTGTTGTTGCTCTCTCCAGGAATCATCTTTACAGATCTCAAAAGAGGCTCTTCAAT 552
536 ACAAGTGTGCAATTTAGCAGAACTCCCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 595
553 ACACCT-----GCAGCTCTCATTTTCCATACAGTCAGTATCAATTTCTGGAAGAATT 603
596 TCTGCTGCTTTAAATGAACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 655
604 TCCAGACATTAAGATAGTCACTTTGGGGTGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
656 TCTATGTGCAATGAGAAACACTA-----AGGTTGAGGAGGAGGATAGGCTGCTGCTGCT 706
664 GCTACTCGGGAACTCTTAAATACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723

707 TTTTCAAGCTTGTGTTTGGCGTAAATGATGATGCTTCTTCTGATGCTGGGGCGCTACAATA 766
724 CTGTGAGGCTTATCTTCCACATCATGATGTTTATTTTCTTCTGCGGCTCCCTACAACA 783
767 TTGCATTTTCTGCTGCTCACTTTTCAAGAACTTTCTCCCTGAGTGACTGCAAGAGCAGCT 826
784 TTGTCCTTCTCTGAAACACCTTCCAGGAATTTCTTGGCTGGAATAATTTGAGTAGCTCTA 843
827 ACAATCTGGACAAAGTGTTCACATCACTAACTCATGCGCCACCACTGCTGCTGCTGCTGCT 886
844 ACAGTTTGGACCAAGCTATGCGGTGACAGAGACTCTTGGGATGACGCACTGCTGCTGCTGCT 903
887 ACCCTCTCTGATGCTGCTTCTTGTGATGGGCAATTTAGCAAACTCTGCTGCGCTGCTTCTCC 946
904 ACCCATCATCTATGCTTCTTGTGCGGGAGAGTTTCAAGAACTTACCTCTTGTGCTTCTTCTCC 963
947 ATCTGCGTAGTAACA 961
964 AAAAGCACATTTGCCA 978

RESULT 9
US-09-087-232A-12
Sequence 12 Application US/09087232A
Patent No. 6153431
GENERAL INFORMATION:
APPLICANT: Quilient et al.
TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/087,232A
FILING DATE: 28 May 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,057
FILING DATE: 30 May 1997
ATTORNEY/AGENT INFORMATION:
NAME: KOLE, LISA B.
REGISTRATION NUMBER: 35,225
REFERENCE/DOCKET NUMBER: AP 31115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2628
TELEFAX: (212) 765-2519
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1376 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 240..1298
US-09-087-232A-12

Query Match 22.3%; Score 230.6; DB 3; Length 1376;
Best Local Similarity 57.0%; Pred. No. 7.2e-65;
Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;

74 CAGAGCAATGTGACAAAGTATGACGCCAGGCACTCTCAGCCAGCTGGTGCATCACTCT 133

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Db 289 CGAGCCCTCCAAAAATCAATGTGAAGCAATCGAGCCCGCTCTCGCTCT 348
Qy 134 GCTCTGCTGTGTGATCGGTGCTCGAACAATCTCTGGTGTGCTTATCTGGTAA 193
Db 349 ACTCACTGGTGTTCATCTTTGGTTTGTGGGCAACATGCTGGTCATCTCATCTGATAA 408
Qy 194 AATATAAGGACTCAAGCGGTGGAAAAATATCTATCTTCTAAACTGGCAGTTCTAACT 253
Db 409 ACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTGTACC 468
Qy 254 TGTGTTCTCTTCTACCTGCTTCCCTTCTGGGCTCATGCTGGGGCG----- 298
Db 469 TGTGTTCTCTTCTACCTGCTTCCCTTCTGGGCTCATGCTGGCCCACTGGGACTTTG 528
Qy 299 ---ATCCATGTGTAAATTTCTCATTTGAGCTGTACTTCTGCTGGGCTGTACAGTGACAT 355
Db 529 GAAATACATGTGTCAACTCTTGACAGGGCTCTATTTATAGGCTTCTTCTCTGGAATCT 588
Qy 356 TTTTCAATTCCTCTGACTGTGCAAGGTACCTAGTGTGTTTGGCAAGGCACTTTT 415
Db 589 TCTTCATCATCTCTGACAAATCGATAGTACCTGGCTGTGCTCATGCTGTGTTGCTT 648
Qy 416 TCTCAGCAGGAGGCTGCTTGGCATCTATTCAAGTGTCTTGGCATGGTAACAG 475
Db 649 TAAAGCC---AGGACGGTCACTTTGGGGTGTGACAGTGTGATCACTTGGGTGG 705
Qy 476 CCATTTCTGGCCACTTTGCTGCTGAAATTCGTGTTTATAAACCCTCAGATGGAAACCAAT 535
Db 706 CTGTGTTGGCTCTCTCCAGGAATCATCTTTACCATGATCTCAAAAGAGGCTTCAAT 765
Qy 536 ACAAGTGTGATTTAGCAGAACTCCCTTCTGCGCAGCTGATGACATCTTGAAGCAT 595
Db 766 ACACCT-----GCAGCTCTCATTTTCCATACAGTCAATCAATCTGGAAGAT 816
Qy 596 TCTGACTTTAAAAATGAACAATTCGGTCTCTGTCTTCCCTCTTATTTTATACATTC 655
Db 817 TCAGACATTTAAGATAGTATCTTGGGGTGTGCTGCTGCTGCTGTGATGTCATCT 876
Qy 656 TCTATGTGCAATAGAGAAAACTA-----AGTTTCAGGGAGCAGAGGTATAGCC 706
Db 877 GCTACTCGGAATCTTAAAAAATCTGCTCGGTGTGAAATGAGAAAGAGGCAAGGG 936
Qy 707 TTTTCAAGCTGTTTGTGCGTATGCTGCTCTCTTCTGATGTGGCGCCCTACAATA 766
Db 937 CTGTGAGGCTTATCTTCCACCATCATGATGTTTATTTCTTCTTCTGCGCTCCCTACAACA 996
Qy 767 TTGCATTTTCTGTCTCACTTTCAAGAAACATTTCTCCCTGAGTGAATGCAAGAGCAGCT 826
Db 997 TTGTCCTTCTCTGMAACCTTCCAGGAATCTTTGGCCTGAAATTTGCAAGTCTTA 1056
Qy 827 ACAATCTGGAACAAAGTGTTCATCATCACTAACTCATCGCCACACCCACTGTGTGATCA 886
Db 1057 ACAGTTGGACCAAGCTATGACAGTGCACAGAGACTTTGGGATGACGCACTGCTGCATCA 1116
Qy 887 ACCCTCTCTGTATGCGTTTCTTGATGGGACATTTAGCAATACCTTGGCGCTGTTTC 946
Db 1117 ACCCCATCATCTATGCTTGTGCGGGAGAAGTTCAGAACTACCTCTTGTCTTCTTCC 1176
Qy 947 ATCTGCTAGTAAACA 961
Db 1177 AAGACATTTGCCA 1191
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RESULT 10

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US-09-016-434-1104
; Sequence 1104, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
```

```
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREMITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1376 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1262810
; US-09-016-434-1104
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Query Match 22.3%; Score 230.6; DB 4; Length 1376;
Best Local Similarity 57.0%; Pred. No. 7.2e-65;
Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;

Qy 74 CAGAGCAATGTGCAAGTATGACGCCAGCAGCTCTCAGCCAGCTGGTCCCATCACTCT 133
Db 289 CGAGCCCTGCCAAAAAATCAATGTGAAGCAATCGAGCCCGCTCTCGCTCGCTCT 348
Qy 134 GCTCTGCTGTGTTGTGATCGGTGTCTCTGACAAATCTCTGGTGTGCTTATCTGTAA 193
Db 349 ACTCACTGGTGTTCATCTTTGTTTGTGGCAACATGCTGGTCATCTCATCTGATAA 408
Qy 194 AATATAAGGACTCAAAAGCGGTGGAAAAATATCTATCTTCTAAACTGGGAGTTCTAACT 253
Db 409 ACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTGTACC 468
Qy 254 TGTGTTCTTCTGCTTACCTCGCCCTCTGGCTCATGCTGGGGCG----- 298
Db 469 TGTGTTCTTCTTCTTCTGCTTCCCTTCTGGGCTCATGCTGCTGCGCCAGTGGACTTTG 528
Qy 299 ---ATCCATGTGTAAAAATTTCTCATTTGAGCTGTACTTCTGGGCTGTGTACAGTGACAT 355
Db 529 GAAATACATGTCTCAACTCTTGACAGGGCTCTATTTATAGGCTTCTTCTCTGGAATCT 588
Qy 356 TTTTCAATTCCTTCTGACTGTGCAAGGTACCTAGTGTGTTTGGCAAGGCACTTTT 415
Db 589 TCTTCATCATCTCTGCAAAATCGATAGTACCTGGCTGTGCTGCTGCTGTTGCTT 648
Qy 416 TCTCAGCAGGAGGCTGCTGCGCATCTATTCAAGTGTCTTGGCATGGTAACAG 475
Db 649 TAAAGCC---AGGACGGTCACTTTTGGGGTGTGACAGTGTGATCACTTGGGTGG 705
Qy 476 CCATTTCTGGCCACTTTGCTGCTGAAATTCGTGTTTATAAACCCTCAGATGGAAACCAAT 535
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Db	706	CTGTGTTTGGCTCTCTCCAGGAATCATCTTTACCAATCTCAAAAAGAGGCTTCTCATTT	765
Qy	536	ACAAGTGTGCATTTAGCAGAACTCCCTTCTCGCCAGCTGATGAGACATTTCTGGAAGCATTT	595
Db	766	ACACCT-----GCAGCTCTCATTTTCCATACAGTCAGTATCAATTTCTGGAAGAATTT	816
Qy	596	TTCTGCATTTTAAATAAGAACATTTTCGGTCTGTGTCTCCCTCATTTTATTTTACATTTTC	655
Db	817	TCCAGACATTTAAAGATAGTCATCTTGGGCTGTCTGTCCGCTCTCTGTCAATGGTCACTCT	876
Qy	656	TCTATGTCAAATGAGAAAAACACTA-----AGGTTTCAGGGAGCAGAGGTATAGCC	706
Db	877	GCTACTCGGGAATCCTAAAAACTCTGCTTCGGTGTTCGAATGAGAAAGAGGCACACGG	936
Qy	707	TTTTCAAGCTGTTTTTTCGGTAAATGATAGTCTCTCTCTGATGTGGCGCCCTACATTA	766
Db	937	CTGTGAGCGTTATCTTCACCAATCANGATGTGTTATTTTCTCTCTCGGGCTCCCTTACAACA	996
Qy	767	TTGCATTTTTTCTCTGCTCCACTTTCAAAGAACACTTCTCCCTCAGTGACTGCAAGAGCAGCT	826
Db	997	TTGTCCCTTCTCCTGAACACCTTCCAGGAATCTTTTGGCCTGAATAATTCAGTAGCTCTA	1056
Qy	827	ACAATCTGGACAAAAGTGTTCACATCACTAAACTCATTCGCCACACCCACTGCTGCATCA	886
Db	1057	ACAGGTTGGACCAAGCTATGCAGGTGACAGAGACTCTTTGGGATGAGCCACTGCTGCATCA	1116
Qy	887	ACCCCTCTCTGTATGCGTGTCTTGTATGGGACATTTTAGCAATAACTCTGCGCGCTGTTTCC	946
Db	1117	ACCCCATCATCTATGCCCTTTGTCTGGGAGAGATTCAGAACTACCTCTTAGTCTTCTTCC	1176
Qy	947	ATCTGCGTAGTAACA	961
Db	1177	AAAAGCACATTGCCA	1191

RESULT 11

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US-09-796-202-2
; Sequence 2, Application US/09796202
; Patent No. 6548636
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULENTED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: human
US-09-796-202-2

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RESIII.T 12

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RES001.12
US-09-502-783A-1
/ Sequence 1, Application US/09502783A
/ Patent No. 6511826
/ GENERAL INFORMATION:
/ APPLICANT: Li, Yi
/ APPLICANT: Ruben, Steven M.
/ TITLE OF INVENTION: Polynucleotides Encodiii
/ TITLE OF INVENTION: HDGNR10
/ FILE REFERENCES: 1488.1150006
/ CURRENT APPLICATION NUMBER: US/09/502,783A
/ CURRENT FILING DATE: 2001-08-23
/ PRIOR APPLICATION NUMBER: 08/466,343
/ PRIOR FILING DATE: 1995-06-06
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: Patent in version 3.0
/ SEQ ID NO 1
/ LENGTH: 1414
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (259)..(1314)

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US-09-502-783A-1

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Query Match      22.3%; Score 230.6; DB 4; Length 1414;
Best Local Similarity 57.0%; Pred. No. 7.3e-65;
Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;

QY 74 CAGAGCAATGTGCAAGTATGAGCCCGCAGGCACTCTCAGGCCAGCTGGTGCCATCACTCT 133
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 367
QY 134 GCTCTGCTGTTTGTGATCGGTGCTCTGGAACAATCTCTGGTGTGCTTATCTGGTAA 193
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 427
QY 194 AATATAAGGACTCAAGCGGTGGAATAATCTATCTTAACTTGGCAGTTTCTAACT 253
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 487
QY 254 TGTGTTTCTTGTCTTACCCCTTCTGGGCTCATGTCTGGGGCG----- 298
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 547
QY 299 ---ATCCCATGTGTAATAATCTCAATTTGGAAGTGTGAGTGTGAGTGTGAGTGTG 355
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 607
QY 356 TTTTCAATTCGCTTCTGACTGTGCAAGGTACTAGTGTGTTTGCACAAGGGCACTTTT 415
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 667
QY 416 TCTCAGCCAGGAGGGGTGCCCTGTGGCATCATTTACAAAGTGTCTCGGCATGGGTAAACAG 475
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 724
QY 476 CCATTCTGGCCACTTTGCTGTGAATTCGTGGTTTATAAACTCAGATGGGAAGACAGAAAT 535
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 784
QY 536 ACAAGTGTGCATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTTCTGGAAGCATT 595
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 835
QY 596 TCTGACTTTAAATAAGCAATTTCCGTTCTTCTCTCCCTTATTTATTTTACATTTTC 655
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 895
QY 836 TCCAGACATTAAGATAGTCACTTGGGGTGTCTCTGGCGCTGCTGTGTCATCT 895
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 896 GCTACTCGGGAATCCTTAAATACTCTGCTGGGTGCGAATGAGAAAGAGGACACAGGG 955
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 74 CAGAGCAATGTGCAAGTATGAGCCCGCAGGCACTCTCAGGCCAGCTGGTGCCATCACTCT 133
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 367
QY 134 GCTCTGCTGTTTGTGATCGGTGCTCTGGAACAATCTCTGGTGTGCTTATCTGGTAA 193
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 427
QY 194 AATATAAGGACTCAAGCGGTGGAATAATCTATCTTAACTTGGCAGTTTCTAACT 253
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 487
QY 254 TGTGTTTCTTGTCTTACCCCTTCTGGGCTCATGTCTGGGGCG----- 298
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 547
QY 299 ---ATCCCATGTGTAATAATCTCAATTTGGAAGTGTGAGTGTGAGTGTGAGTGTG 355
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 607
QY 356 TTTTCAATTCGCTTCTGACTGTGCAAGGTACTAGTGTGTTTGCACAAGGGCACTTTT 415
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 667
QY 416 TCTCAGCCAGGAGGGGTGCCCTGTGGCATCATTTACAAAGTGTCTCGGCATGGGTAAACAG 475
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 724
QY 476 CCATTCTGGCCACTTTGCTGTGAATTCGTGGTTTATAAACTCAGATGGGAAGACAGAAAT 535
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 784
QY 536 ACAAGTGTGCATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTTCTGGAAGCATT 595
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 835
QY 596 TCTGACTTTAAATAAGCAATTTCCGTTCTTCTCTCCCTTATTTATTTTACATTTTC 655
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 895
QY 836 TCCAGACATTAAGATAGTCACTTGGGGTGTCTCTGGCGCTGCTGTGTCATCT 895
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 896 GCTACTCGGGAATCCTTAAATACTCTGCTGGGTGCGAATGAGAAAGAGGACACAGGG 955
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 74 CAGAGCAATGTGCAAGTATGAGCCCGCAGGCACTCTCAGGCCAGCTGGTGCCATCACTCT 133
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 367
QY 134 GCTCTGCTGTTTGTGATCGGTGCTCTGGAACAATCTCTGGTGTGCTTATCTGGTAA 193
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 427
QY 194 AATATAAGGACTCAAGCGGTGGAATAATCTATCTTAACTTGGCAGTTTCTAACT 253
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 487
QY 254 TGTGTTTCTTGTCTTACCCCTTCTGGGCTCATGTCTGGGGCG----- 298
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 547
QY 299 ---ATCCCATGTGTAATAATCTCAATTTGGAAGTGTGAGTGTGAGTGTGAGTGTG 355
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 607
QY 356 TTTTCAATTCGCTTCTGACTGTGCAAGGTACTAGTGTGTTTGCACAAGGGCACTTTT 415
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 667
QY 416 TCTCAGCCAGGAGGGGTGCCCTGTGGCATCATTTACAAAGTGTCTCGGCATGGGTAAACAG 475
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 724
QY 476 CCATTCTGGCCACTTTGCTGTGAATTCGTGGTTTATAAACTCAGATGGGAAGACAGAAAT 535
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 784
QY 536 ACAAGTGTGCATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTTCTGGAAGCATT 595
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 835
QY 596 TCTGACTTTAAATAAGCAATTTCCGTTCTTCTCTCCCTTATTTATTTTACATTTTC 655
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 895
QY 836 TCCAGACATTAAGATAGTCACTTGGGGTGTCTCTGGCGCTGCTGTGTCATCT 895
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QY 896 GCTACTCGGGAATCCTTAAATACTCTGCTGGGTGCGAATGAGAAAGAGGACACAGGG 955
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RESULT 13

US-09-502-784A-1

Qy 707 TTTTCAAGCTTGTGTTTGGCGTAATGGTAGTCTTCTTCTGATGTGGGCGCTTACAATA 766
Db 956 CTGTGAGGCTTATCTTCAACATCATGATGTTGTTATTTCTTCTTGGGCTCCCTTACAACA 1015
Qy 767 TTGCATTTTCTCTGTCACATTTTCAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCT 826
Db 1016 TTGTGCTTCTCTGAAACACTTTCAGGAAATTTCTTGGCCTGAAATTAATGCAAGTACTTA 1075
Qy 827 ACAATCTGGACAAAGTGTTCACATCACTAACTCATCGCCACACCCACTGCTGCATCA 886
Db 1076 ACAGTTGGACCAAGCTATGAGGTGACAGAGACTCTTGGATGACGCACTGCTGCATCA 1135
Qy 887 ACCCTCTCTGTATGCGTTTCTGATGGGACATTTAGCAAAATACCTCTGCGGCTGTTTCC 946
Db 1136 ACCCATCATCTATGCGCTTTGTGCGGGAAGTTTCAAGAACTACCTCTTAGTCTTCTTCC 1195
Qy 947 ATCTGCGTAGTAACA 961
Db 1196 AAAAGCACATTGCCA 1210

RESULT 14

US-09-339-912A-1
; Sequence 1, Application US/09339912A
; Patent No. 6759519
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10
; FILE OF INVENTION: CCR5 Receptor
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/339,912A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (259)..(1314)
; OTHER INFORMATION: Description of Artificial Sequence: Genomic
US-09-339-912A-1

Query Match 22.3%; Score 230.6; DB 4; Length 1414;
Best Local Similarity 57.0%; Pred. No. 7.3e-65;
Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;
Qy 74 CAGAGCAATGTGACAGTATGACCCGACCTCTCAGCCAGCTGTGGCCATCATCT 133
Db 308 CGGAGCCCTCGCAAAAATCAATGTGAAGCAATCGCAGCCGCTCTCGCTCGCTCT 367
Qy 134 GCTCTGCTGTGTTGTGATCGGTCTCTGACATCTCTCGGTGTGCTTATCTGTGTA 193
Db 368 ACTCAGTGGTGTTCATCTTTGGTTTGTGGGCAACATGCTGTGTCATCTCATCTGATA 427
Qy 194 AATATAAGGACTCAACGCGTGGAAATATCTATCTTAACTTGGCAGTTTCTAACT 253
Db 428 ACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTGACC 487
Qy 254 TGTGTTTCTTCTTACCTGCTTCTGCGGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 298
Db 488 TGTGTTTCTTCTTACCTGCTTCTGCGGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 547
Qy 299 ----ATCCCATGTGAAAAATTTCTGAGCTGATCTGCTGCGGCTGTACAGTACAT 355
Db 548 GAAATACAAATGTGCAACTCTTGACAGGCTCTATTTTATAGGCTTCTTCTCTGGAATCT 607

Qy 356 TTTTCAATGCTTCTGACTGTGCAAGGTACCTAGTGTGTTTGGCAAGGGCAACTTTT 415
Db 608 TCTTCATCATCTCTCTGACAAATCGATAGGTACCTGGCTGCTGCTCATGCTGTGTTGCTT 667
Qy 416 TCTCAGCAGGAGGAGGCTGCTGCGCATCATTAAGTGTCTGCAAGTGGGTAAACAG 475
Db 668 TAAAGCC----AGACCGTCACTTTGGGGTGTGACAGTGTGATCACTTGGGTGGTG 724
Qy 476 CCATTTCTGGCCACTTTGCTGAAATTCGTGTTTATAAACCTCAGATGAAAGACAGAAAT 535
Db 725 CTGTGTTGGCTCTCTCCCAAGGAATCATCTTTACCAGATCTCAAAAAGAGGCTTTCATT 784
Qy 536 ACAAGTGTGATTTAGCAGAACTCCCTTCTGCGCAGCTGATGAGACATTTCTGGAAGCAT 595
Db 785 ACACCT-----GCAGCTCTCATTTTCCATACAGTCAGTATCAATTTCTGGAAGAAAT 835
Qy 596 TTCTGACTTTTAAAAATGAACATTTCCGTTTCTGCTCCCTCCCTATTTATTTTACATTTT 655
Db 836 TCAGACATTAAGATAGTCACTTTGGGGCTGGTCTGCGCGCTGCTTGTATGTCATCT 895
Qy 656 TCTATGTGCAATGAGAAAAACACTA-----AGTTTCAGGGAGCAGAGGTATAGCC 706
Db 896 GCTACTCGGAATCCTTAAAACTCTGCTTGGTGTGAAATGAGAAGAGGACACAGG 955
Qy 707 TTTTCAAGCTTGTGTTTGGCGTAATGGTAGTCTTCTTCTGATGTGGGCGCTTACAATA 766
Db 956 CTGTGAGGCTTATCTTCAACCATCATGATGTTTATTTTCTTCTGCGGCTCCCTTACAACA 1015
Qy 767 TTGCATTTTCTGCTCCACTTTTCAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCT 826
Db 1016 TTGTCTTCTTCTGAAACACTTCCAGGAATTTCTTGGCCTGAAATTAATGCAAGTACTTA 1075
Qy 827 ACAATCTGGACAAAGTGTTCACATCACTAACTCATCGCCACCCACTGCTGCATCA 886
Db 1076 ACAGTTGGACCAAGCTATGAGGTGACAGAGACTCTTGGATGACGCACTGCTGCATCA 1135
Qy 887 ACCCTCTCTGTATGCGTTTCTTGTGAGGAGCATTTAGCAAAATACCTCTGCGGCTGTTTCC 946
Db 1136 ACCCATCATCTATGCTTGTGCGGGAAGTTTCAAGAACTACCTCTTAGTCTTCTTCC 1195
Qy 947 ATCTGCGTAGTAACA 961
Db 1196 AAAAGCACATTGCCA 1210

RESULT 15

US-09-195-662A-1
; Sequence 1, Application US/09195662A
; Patent No. 6800729
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGNR10 (CCR5 Receptor)
; FILE REFERENCE: 1488.1150002
; CURRENT APPLICATION NUMBER: US/09/195,662A
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (259)..(1314)
; OTHER INFORMATION: Description of Artificial Sequence: Genomic
US-09-195-662A-1

Query Match 22.3%; Score 230.6; DB 4; Length 1414;
Best Local Similarity 57.0%; Pred. No. 7.3e-65;


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Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;
Qy 74 CAGAGCAATGTGACGATGAGCCAGGCACTCTCAGCCAGCTGGTGGCCATCACTCT 133
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 308 CGGAGCCCTGCCAAAATCAATGTGAAGCAAAATCGCAGCCCGCTCTCCCTCCGCTCT 367
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 134 GCTCTGCTGTGTGATCGGTGCTCCTGGACAAATCTCCTGGTGTGCTTATCTGTGTA 193
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 368 ACTCAGTGTGTTCATCTTTGGTGTGTTGGCAACATGCTGCTCATCTCTGATAA 427
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 194 AATATAAGGACTCAAAAGGTTGAAATATCTATCTTTAAACTTTGGCAGTTTCTAACT 253
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 428 ACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGTCAACCTGGCCATCTCTGACC 487
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 254 TGTGTTTCTTGTCTTACCTCGCTTCTGGGCTCATGCTGGGGGG----- 298
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 488 TGTGTTTCTTGTCTTACCTCGCTTCTGGGCTCATGCTGGGGGGGGGGGGGGGG 547
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 299 ---ATCCCATGTGTAAATTTCTCATTTGGACTGTACTTCGTGGGCTGTACAGTGAGACAT 355
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 548 GAAATACAATGTGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTTGGATCT 607
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 356 TTTTCAATGCCCTCTGACTGTGCAAGGTAAGTCTAGTGTGTTTGGCAAGGGCAACTTTT 415
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 608 TCTTCATCATCTCTGACAAATGATAGGTACCTGGCTGCTGCTCCATGCTGTGTGCTT 667
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 416 TCTCAGCCAGGAGGGTGGCTTGGCATCATACAGTGTCTTGGCATGGTAAACAG 475
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Qy 668 TAAAGGCC---AGGACGGTCACTTTGGGGTGGTGAAGTGTGATCACTTGGGTGGTGG 724
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 476 CCATTTCTGGCCACTTTGCCCTGAATTCGTGGTGTATTAACCTCAGATGGAAGACAGAAAT 535
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Qy 725 CTGTGTTGGCTCTCTCCAGGAATCATCTTACCAGATCTCAAAAAGAGGTCTTCATT 784
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 536 ACAAGTGTGCAATTAGCAGAACTCCCTTCTGCGAGCTGATGAGACATTTCTGGAAGCAT 595
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Qy 785 ACACCT-----GCAGCTCTCATTTTCCATACAGTCAGTATCAATTTCTGGAAGAAAT 835
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 596 TTCTGACTTTTAAATTAACATTTGGTCTTGTGCTCCCTCTATTTTATTTTACATTTC 655
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 836 TCCAGACATTAAGATAGTCACTTGGGGTGGTCTGCGCTGCTTGTCTATGGTCACT 895
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 656 TCTATGTGCAAAATGAGAAAACACTA-----AGTTTCAGGGAGCAGAGGTATAGCC 706
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 896 GCTACTCGGGAATCCTAAAACCTTGCTCGGTGCGAATGAGAGAAGAGGCAAGGG 955
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 707 TTTTCAAGCTTGTGTTTGGCGTAATGTAGTCTTCTTCTGATGTGGGGCCCTACAATA 766
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 956 CTGTGAGGCTTATCTTCAACATCATGATGTTTATTTTCTTCTGCGGCTCCCTACAACA 1015
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 767 TTGCATTTTCTGTCACCTTCAAGAACACTTCTCCCTGAGTGAAGTGAAGAGCAGCT 826
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1016 TTGTCCTTCTCCTGAACACCTTCAGGAATTTCTTTGGCCTGAATAATTGCAGTAGCTCTA 1075
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 827 ACAATCTGGAACAAAGTGTTCACATCACTAACTCATGCGCACCCACTGCTGCATCA 886
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Qy 1076 ACAGTTGGACCAAGCTATGAGGTGACAGAGACTCTTGGGATGACGCACTGCTGCATCA 1135
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 887 ACCCTCTCCTGATGCGTTTCTTGAAGGACATTTAGCAAAATACCTTCTCCGCTGTTTCC 946
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1136 ACCCATCATCTATGCTTGTGCGGGAGAAGTTCAAGAACTACCTCTTAGTCTTCTTCC 1195
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Qy 947 ATCTGCGTAGTAACA 961
Db ||||| ||||| |||||
Qy 1196 AAAAGCACATTGGCA 1210
Db ||||| ||||| |||||
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Search completed: June 18, 2005, 12:14:47
Job time : 203.888 secs


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QY 181 CTTATCTCGTAAATATATAAGGACTCAACCGCGTGGAAATATCTATCTCTAAACTTG 240
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QY 241 GCAGTTTCTAACTGCTGTTCTTCTGTTACCTCGCCCTTCTGGGCTCATGCTGGGGCGAT 300
Db 325 GCAGTTTCTAACTGCTGTTCTTCTGTTACCTCGCCCTTCTGGGCTCATGCTGGGGCGAT 384
QY 301 CCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGGGCTGTACAGTGAGACATTTTTTC 360
Db 385 CCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGGGCTGTACAGTGAGACATTTTTTC 444
QY 361 AATTGCCCTTCTGACTGTGCAAGGTACCTAGTGTGTTTTTGGCAAGGGCAACTTTTTCTCA 420
Db 445 AATTGCCCTTCTGACTGTGCAAGGTACCTAGTGTGTTTTTGGCAAGGGCAACTTTTTCTCA 504
QY 421 GCCAGGAGGGTCCCTGTGGCATCAATCAAGTGTCTGGCATGGTAAACGCCAATT 480
Db 505 GCCAGGAGGGTCCCTGTGGCATCAATCAAGTGTCTGGCATGGTAAACGCCAATT 564
QY 481 CTGGCCACTTTGCCCTGAATTCGTGGTTTATAAACCTCAGATGGAAGACCAAGATACAAG 540
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QY 541 TGTGCAATTTAGCAGAACTCCCTTCTGCGAGCTGATGAGACATTTCTGAAGCATTTTCTG 600
Db 625 TGTGCAATTTAGCAGAACTCCCTTCTGCGAGCTGATGAGACATTTCTGAAGCATTTTCTG 684
QY 601 ACTTTAAATAATGACATTTCCGTTCTCTCCCTTATTTTATTTTACATTTCTCTAT 660
Db 685 ACTTTAAATAATGACATTTCCGTTCTCTCCCTTATTTTATTTTACATTTCTCTAT 744
QY 720 GTGCAATGAGAAAAACAATAAGTTTCAAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 780
Db 804 GTGCAATGAGAAAAACAATAAGTTTCAAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 864
QY 780 TTTGCGTAATGAGTGTCTCTTCTGATGTGGGGCCCTCAATATTTGCAATTTTCTG 840
Db 864 TTTGCGTAATGAGTGTCTCTTCTGATGTGGGGCCCTCAATATTTGCAATTTTCTG 884
QY 840 TCCACTTTCAAGAACACTTCTCCCTGAGTGCATGCAAGAGCAGCTACAATCTGACAAA 900
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QY 900 AGTGTTCACATCACTAACTCATCGCCACCACTCTGTCATCAACCCCTCTCTGTAT 960
Db 984 AGTGTTCACATCACTAACTCATCGCCACCACTCTGTCATCAACCCCTCTCTGTAT 1044
QY 960 GCGTTTCTTGATGGACATTTAGCAAAATACCTCTGCGCTGTTTCCATCTCGGTAGAAC 1020
Db 1044 GCGTTTCTTGATGGACATTTAGCAAAATACCTCTGCGCTGTTTCCATCTCGGTAGAAC 1104
QY 1021 TCCACCGAAGTGTA 1035
Db 1105 TCCACCGAAGTGTA 1119
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RESULT 3

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US-10-754-071-11
; Sequence 11, Application US/10754071
; Publication No: US20040137578A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Wei
; APPLICANT: Gish, Kurt C.
; APPLICANT: Schall, Thomas J.
; APPLICANT: Vicari, Alain P.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Chemokine TECK Polypeptides
; FILE REFERENCE: DX0589K1C US
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; CURRENT APPLICATION NUMBER: US/10/754,071
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 10/039,659
; PRIOR FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: US 08/887,977
; PRIOR FILING DATE: 1997-07-03
; PRIOR APPLICATION NUMBER: US 60/021,664
; PRIOR FILING DATE: 1996-07-05
; PRIOR APPLICATION NUMBER: US 60/028,329
; PRIOR FILING DATE: 1996-10-11
; PRIOR APPLICATION NUMBER: US 60/048,593
; PRIOR FILING DATE: 1997-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (49)..(1116)
; OTHER INFORMATION:
US-10-754-071-11
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Query Match 100.0%; Score 1035; DB 19; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGCCCAATTACACGCTGGCACAGAGGATGAATATATGATGTCCTCATAGAGGTGAACCTG 60
Db 85 ATGCCCAATTACACGCTGGCACAGAGGATGAATATATGATGTCCTCATAGAGGTGAACCTG 144
QY 61 GAGAGCGATGAGGAGAGCAATGTGACAAAGTATGACGCCAGGCACTCTCAGCCCAGCTG 120
Db 145 GAGAGCGATGAGGAGAGCAATGTGACAAAGTATGACGCCAGGCACTCTCAGCCCAGCTG 204
QY 121 GTGCCATCACTCTCTCTGCTGTTGTGATCGGTGTCTGGCAATATCTCTCTGTTGTG 180
Db 205 GTGCCATCACTCTCTCTGCTGTTGTGATCGGTGTCTGGCAATATCTCTCTGTTGTG 264
QY 181 CTTATCTCGTAAATATATAAGGACTCAACCGCGTGGAAATATCTATCTCTAAACTTG 240
Db 265 CTTATCTCGTAAATATATAAGGACTCAACCGCGTGGAAATATCTATCTCTAAACTTG 324
QY 241 GCAGTTTCTAACTGCTGTTCTTCTTACCTCGCCCTTCTGGGCTCATGCTGGGGCGAT 300
Db 325 GCAGTTTCTAACTGCTGTTCTTCTTACCTCGCCCTTCTGGGCTCATGCTGGGGCGAT 384
QY 301 CCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGGGCTGTACAGTGAGACATTTTTTC 360
Db 385 CCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGGGCTGTACAGTGAGACATTTTTTC 444
QY 361 AATTGCCCTTCTGACTGTGCAAGGTACCTAGTGTGTTTTTGGCAAGGGCAACTTTTTCTCA 420
Db 445 AATTGCCCTTCTGACTGTGCAAGGTACCTAGTGTGTTTTTGGCAAGGGCAACTTTTTCTCA 504
QY 421 GCCAGGAGGGTCCCTGTGGCATCAATCAAGTGTCTGGCATGGTAAACGCCAATT 480
Db 505 GCCAGGAGGGTCCCTGTGGCATCAATCAAGTGTCTGGCATGGTAAACGCCAATT 564
QY 481 CTGGCCACTTTGCCCTGAATTTCTGTTTATAAACCTCAGATGGAAGACCAAGATACAAG 540
Db 565 CTGGCCACTTTGCCCTGAATTTCTGTTTATAAACCTCAGATGGAAGACCAAGATACAAG 624
QY 541 TGTGCAATTTAGCAGAACTCCCTTCTGCGAGCTGATGAGACATTTCTGAAGCATTTTCTG 600
Db 625 TGTGCAATTTAGCAGAACTCCCTTCTGCGAGCTGATGAGACATTTCTGAAGCATTTTCTG 684
QY 601 ACTTTAAATAATGACATTTCCGTTCTCTCCCTTATTTTATTTTACATTTCTCTAT 660
Db 685 ACTTTAAATAATGACATTTCCGTTCTCTCCCTTATTTTATTTTACATTTCTCTAT 744
QY 661 GTGCAATGAGAAAAACAATAAGTTTCAAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 720
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Db 745 GTGCAATGAGAAAAACACTAAGGTTTCAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 804
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Qy 781 TCCACTTTTCAAGAAACACTTTCTCCCTGAGTGACTGCAAGAGCAGCTACAAATCTGGACAA 840
Db 865 TCCACTTTTCAAGAAACACTTTCTCCCTGAGTGACTGCAAGAGCAGCTACAAATCTGGACAA 924
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Qy 901 GCGTTTCTGATGGGACATTTAGCAATACCTCTGCGGCTGTTTCATCTGCGTAGTAAC 960
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Qy 1021 TCCACCGAAGTGTA 1035
Db 1105 TCCACCGAAGTGTA 1119

RESULT 4

US-10-759-860-11
; Sequence 11, Application US/10759860
; Publication No. US20050074790A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Wei
; APPLICANT: Gish, Kurt C.
; APPLICANT: Schall, Thomas J.
; APPLICANT: Vicari, Alain P.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods for using chemokine TECK
; FILE REFERENCE: DX0589KID US
; CURRENT APPLICATION NUMBER: US/10759,860
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 10/039,659
; PRIOR FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: US 08/887,977
; PRIOR FILING DATE: 1997-07-03
; PRIOR APPLICATION NUMBER: US 60/021,664
; PRIOR FILING DATE: 1996-07-05
; PRIOR APPLICATION NUMBER: US 60/028,329
; PRIOR FILING DATE: 1996-10-11
; PRIOR APPLICATION NUMBER: US 60/048,593
; PRIOR FILING DATE: 1997-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (49)..(1116)
; OTHER INFORMATION:
US-10-759-860-11

Query Match 100.0%; Score 1035; DB 21; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCCCAATTACAGCTGGCACCAGAGGATGAATATGATCTCTCATAGAGGTGAAC 60
Db 85 ATGCCCAATTACAGCTGGCACCAGAGGATGAATATGATCTCTCATAGAGGTGAAC 144
Qy 61 GAGAGCGATGAGGAGAGCAATGTGACAAATATGACGCCCGAGGCACTCTCAGCCGAGCTG 120

Db 145 GAGAGCGATGAGGAGAGCAATGTGACAAAGTATAGCCCGAGGCACTCTCAGCCGAGCTG 204
Qy 121 GTGCCATCACTCTGCTCTGCTGTTGATCGGTGCTCTGGACAATCTCTCGTGTGTG 180
Db 205 GTGCCATCACTCTGCTCTGCTGTTGATCGGTGCTCTGGACAATCTCTCGTGTGTG 264
Qy 181 CTTATCTCTGTAATAATATAAGGACTCAAAACGCGTGGAAAAATATCTATCTTTAAACTTG 240
Db 265 CTTATCTCTGTAATAATATAAGGACTCAAAACGCGTGGAAAAATATCTATCTTTAAACTTG 324
Qy 241 GCAGTTTCTAACTGTGTTTCTGCTTACCTGCTCTCTGGGCTCATGCTGGGGGGGAT 300
Db 325 GCAGTTTCTAACTGTGTTTCTGCTTACCTGCTCTCTGGGCTCATGCTGGGGGGGAT 384
Qy 301 CCCATGTGTAATAATCTCATTTGAGTACTTCTGCTGGGCTGTACAGTGAGACATTTTTC 360
Db 385 CCCATGTGTAATAATCTCATTTGAGTACTTCTGCTGGGCTGTACAGTGAGACATTTTTC 444
Qy 361 AATTGCTTCTGACTGTGCAAAAGGTACTAGTGTGTTTTTGCACAAGGGCAACTTTTCTCA 420
Db 445 AATTGCTTCTGACTGTGCAAAAGGTACTAGTGTGTTTTTGCACAAGGGCAACTTTTCTCA 504
Qy 421 GCAGAGGAGGAGTGCCTGTGTCATCAATAAAGTGTCTGTCATGGGTAAACAGCAATT 480
Db 505 GCAGAGGAGGAGTGCCTGTGTCATCAATAAAGTGTCTGTCATGGGTAAACAGCAATT 564
Qy 481 CTGGCCACTTTGCCTGAATTCGTGGTGTATTAACCTCAGATGGAACACAGCAATAACAAG 540
Db 565 CTGGCCACTTTGCCTGAATTCGTGGTGTATTAACCTCAGATGGAACACAGCAATAACAAG 624
Qy 541 TGTGCAATTTAGCAGAACTCCCTTCTGCGCAGCTGATGAGACATTTCTGGAAGCAATTTCTG 600
Db 625 TGTGCAATTTAGCAGAACTCCCTTCTGCGCAGCTGATGAGACATTTCTGGAAGCAATTTCTG 684
Qy 601 ACTTTAAAAATGAAACATTTGCTGCTCCCTTATTTATTTTACATTTCTCTAT 660
Db 685 ACTTTAAAAATGAAACATTTGCTGCTCCCTTATTTATTTTACATTTCTCTAT 744
Qy 661 GTGCAATGAGAAACACTAAGGTTTCAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 720
Db 745 GTGCAATGAGAAACACTAAGGTTTCAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 804
Qy 721 TTTGCGCTAATGGTAGTCTTCTCTGATGTGGGCGCCCTACAATATTGCAATTTTCCCTG 780
Db 805 TTTGCGCTAATGGTAGTCTTCTCTGATGTGGGCGCCCTACAATATTGCAATTTTCCCTG 864
Qy 781 TCACATTTCAAAGAAACACTTTCTCCCTGAGTGACTGCAAGAGCAGCTACAAATCTGGACAA 840
Db 865 TCACATTTCAAAGAAACACTTTCTCCCTGAGTGACTGCAAGAGCAGCTACAAATCTGGACAA 924
Qy 841 AGTGTTCACATCACTAACTCATGCGCACCCACTGCTGTCATCAACCTCTCTCTGTAT 900
Db 925 AGTGTTCACATCACTAACTCATGCGCACCCACTGCTGTCATCAACCTCTCTCTGTAT 984
Qy 901 GCGTTTCTTGTAGGGACATTTAGCAATATACCTCTGCGGCTGTTTCCATCTCGCTAGTAAC 960
Db 985 GCGTTTCTTGTAGGGACATTTAGCAATATACCTCTGCGGCTGTTTCCATCTCGCTAGTAAC 1044
Qy 961 ACCCCACTTCAACCCAGGGGGAGTCTGCAAGGACACATCGAGGGAAGAACCTGACCAT 1020
Db 1045 ACCCCACTTCAACCCAGGGGGAGTCTGCAAGGACACATCGAGGGAAGAACCTGACCAT 1104
Qy 1021 TCCACCGAAGTGTA 1035
Db 1105 TCCACCGAAGTGTA 1119

RESULT 5

US-10-741-600-12
; Sequence 12, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:

```

; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1646
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-12

```

Query Match	99.7%	Score 1032.2	DB 21	Length 1646
Best Local Similarity	99.3%	Pred. No. 0		
Matches 1028	Conservative 7	Mismatches 0	Indels 0	Gaps 0
Qy	1	ATGCCAATTACACGCTGGCACAGAGGATGAATATGATGTGCTCATAGAGGTGAAC	60	
Db	202	ATGCCAATTTCACGCTGGCACAGAGGATGAATGATGTGCTCATAGAGGTGAAC	261	
Qy	61	GAGAGCGATGAGGCAGAGCAATGTGACAAGTATGACGCCACAGGCACCTCAGAGCCAGCTG	120	
Db	262	GAGAGCGATGAGGCAGAGCAATGTGACAAGTATGACGCCACAGGCACCTCAGAGCCAGCTG	321	
Qy	121	GTGCCATCAGCTCTGCTGTGTTTGTGTATCGGTGTCTTGGACAATCTCTGCTGTGTG	180	
Db	322	GTGCCATCAGCTCTGCTGTGTTTGTGTATCGGTGTCTTGGACAATCTCTGCTGTGTG	381	
Qy	181	CTTATCTGTTAAATATAAAGGACTCAAGCGCTGGAAATATCTATCTCTTAAACTTG	240	
Db	382	CTTATCTGTTAAATATAAAGGACTCAAGCGCTGGAAATATCTATCTCTTAAACTTG	441	
Qy	241	GCAGTTTCTAACTTGTTGTTCTGCTTACCCCTGCTCTGGGCTCATGCTGGGGCGAT	300	
Db	442	GCAGTTTCTAACTTGTTGTTCTGCTTACCCCTGCTCTGGGCTCATGCTGGGGCGAT	501	
Qy	301	CCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGTGGGCCCTGTACAGTGAGACATTTTTC	360	
Db	502	CCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGTGGGCCCTGTACAGTGAGACATTTTTC	561	
Qy	361	AATTGCCCTCTGACTGTGCAAGGTAAGTGTGTTTTTGTGCACAAGGGCACTTTTCTCA	420	
Db	562	AATTGCCCTCTGACTGTGCAAGGTAAGTGTGTTTTTGTGCACAAGGGMACTTTTCTCA	621	
Qy	421	GCACGAGGAGGGTCCCTGTGGCATCATTTACAAGTGTCTCGCATGGGTAAACGCATT	480	
Db	622	GCACGAGGAGGGTCCCTGTGGCATCATTTACAAGTGTCTCGCATGGGTAAACGCATT	681	
Qy	481	CTGGCCACTTTGCTGAAATTCGTGGTTTATAAACTCAGATGGAAGACACAGAAATACAAG	540	
Db	682	CTGGCCACTTTGCTGAAATTCGTGGTTTATAAACTCAGATGGAAGACACAGAAATACAAG	741	
Qy	541	TGTGCAATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTTCTGGAAGCATTTTCTG	600	
Db	742	TGTGCAATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTTCTGGAAGCATTTTCTG	801	
Qy	601	ACTTTAAAAATGAACATTTCCGTTCTTGTCTCCCTCATTTATTTTACATTTCTCTAT	660	
Db	802	ACTTTAAAAATGAACATTTCCGTTCTTGTCTCCCTCATTTATTTTACATTTCTCTAT	861	
Qy	661	GTGCAATGAGAAAAACACTAAGGTTTCAGGSAGCAGAGGTATAGCCTTTTCAGAGCTTGT	720	
Db	862	GTGCAATGAGAAAAACACTAAGGTTTCAGGSAGCAGAGGTATAGCCTTTTCAGAGCTTGT	921	
Qy	721	TTTGGCCGTAATGGTAGTCTTCTTCTGATGTGGGCGCCCTACAATATTGCAATTTTCTCG	780	
Db	922	TTTGGCCGTAATGGTAGTCTTCTTCTGATGTGGGCGCCCTACAATATTGCAATTTTCTCG	981	
Qy	781	TCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTACAATCTCGACAAA	840	
Db	982	TCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTACAATCTCGACAAA	1041	

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RESULT 6
US-10-741-600-13
; Sequence 13, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741.600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-13

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Query Match	99.7%	Score 1032.2	DB 21	Length 1776	
Best Local Similarity	99.3%	Pred. No. 0			
Matches 1028	Conservative	7	Mismatches 0	Indels 0	
Qy	1	ATGGCCAA	TACACGCTGGCACCAGAGGATGAATATGATGCTCCTCATAGAGGTGAAC	60	
Db	328	ATGGCCAA	TTTTCACGCTGGCACCAGAGGATGAATATGATGCTCCTCATAGAGGTGAAC	387	
Qy	61	GAGAGCGA	TGAGCAGAGCAATGTGACCAAGTATGACGCCACGACACTCTCAGCCAGCTG	120	
Db	388	GAGAGCGA	TGAGCAGAGCAATGTGACCAAGTATGACGCCACGACACTCTCAGCCAGCTG	447	
Qy	121	GTGCCAT	CACCTCGCTCTGCTGTGTTTGTGATCGGTCTCTGGACAATCTCCTGTTTGTG	180	
Db	448	GTGCCAT	CACCTCGCTCTGCTGTGTTTGTGATCGGTCTCTGGACAATCTCCTGTTTGTG	507	
Qy	181	CTTATCT	TGTTAAATATATAAGGACTCAAA	CGGTGGAATAATCTATCTTTCTAAACTTG	240
Db	508	CTTATCT	TGTTAAATATATAAGGACTCAAA	CGGTGGAATAATCTATCTTTCTAAACTTG	567
Qy	241	GCAGTTT	CTTAACTTGTGTTTCTTTCCTACCCCTGCCCTTCTGGGCTCATGCTGGGGCGAT	300	
Db	568	GCAGTTT	CTTAACTTGTGTTTCTTTCCTACCCCTGCCCTTCTGGGCTCATGCTGGGGCGAT	627	
Qy	301	CCCATGT	TGTAATAATCTCATTTGGACTGTACTCTCGTGGGCCCTGTACAGTGAGACATTTTTC	360	
Db	628	CCCATGT	TGTAATAATCTCATTTGGACTGTACTCTCGTGGGCCCTGTACAGTGAGACATTTTTC	687	
Qy	361	AAATTGC	CTTCTGACTGTGCAAAGGTACTAGTGTTTTTTGACAGGGCAACTTTTTTCTCA	420	
Db	688	AAATTGC	CTTCTGACTGTGCDAAGGTACTAGTGTTTTTTGACAGGGCAACTTTTTTCTCA	747	
Qy	421	GCCAGAG	GAGGTGCCCTGTGGCATCATTTACAAGTGTCTCTGGCATGGGTAAACGCCATT	480	
Db	748	GCCAGAG	GAGGTGCCCTGTGGCATCATTTACAAGTGTCTCTGGCATGGGTAAACGCCATT	807	

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QY 481 CTGCCACATTTGCTGAATTCGTGGTTTATAAAACCTCAGATGGAAGACAGAAATACAAG 540
Db 808 CTGGCCACTTTGCTGAATTCWRTGGTTTATTAACCTCAGATGGAAGACAGAAATACAAG 867
QY 541 TGTGCATTTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTCCTGGAAGCATTTTCTG 600
Db 868 TGTGCATTTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTCCTGGAAGCATTTTCTG 927
QY 601 ACTTTAAATAATGAACATTTTCGGTTCCTGCTCCCTCTATTTATTTTACATTTCTCTAT 660
Db 928 ACTTTAAATAATGAACATTTTCGGTTCCTGCTCCCTCTATTTATTTTACATTTCTCTAT 987
QY 661 GTGCAATGAGAAACACATTAAGGTTTCAGGAGCAGAGGTATAGCCCTTTCAAGCTTGT 720
Db 988 GTGCAATGAGAAACACATTAAGGTTTCAGGAGCAGAGGTATAGCCCTTTCAAGCTTGT 1047
QY 721 TTTGCCGTAAATGTTAGTCTTCTCTGATGTTGGGCGCCCTACAATATTTGCAATTTTCCCTG 780
Db 1048 TTTGCCGTAAATGTTAGTCTTCTCTGATGTTGGGCGCCCTACAATATTTGCAATTTTCCCTG 1107
QY 781 TCCACTTTCAAGAACACATTTCTCCCTGAGTGACTGCAAGAGCAGCTACAACTCTGGACAA 840
Db 1108 TCCACTTTCAAGAACACATTTCTCCCTGAGTGACTGCAAGAGCAGCTACAACTCTGGACAA 1167
QY 841 AGTGTTCACATCACTAAACTCATCGCCACCACCACTGCTGCATCAACCCCTCTCCTGTAT 900
Db 1168 AGTGTTCACATCACTAAACTCATCGCCACCACCACTGCTGCATCAACCCCTCTCCTGTAT 1227
QY 901 GCCTTTCTTGATGGACATTTAGCAATACCTCTGCGCTGTTTCCATCTGCGTAGTAAC 960
Db 1228 GCCTTTCTTGATGGACATTTAGCAATACCTCTGCGCTGTTTCCATCTGCGTAGTAAC 1287
QY 961 ACCCCACTTCAACCCAGGGGGAGTCTGCAAGAGGCATCGAGGGAAGAACCTTGACCAT 1020
Db 1288 ACCCCACTTCAACCCAGGGGGAGTCTGCAAGAGGCATCGAGGGAAGAACCTTGACCAT 1347
QY 1021 TCCACCGAAGTGTA 1035
Db 1348 TCCACCGAAGTGTA 1362
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RESULT 7

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US-10-741-600-17557
; Sequence 17557, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17557
; LENGTH: 14341
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-17557
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Query Match 99.7%; Score 1032.2; DB 21; Length 14341;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1028; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCCAATTACGCTGGCACCAGAGGATGAATATGATGCTCTCATAGAGGTGAACCTG 60
Db 6892 ATGCCCAATTACGCTGGCACCAGAGGATGAATATGATGCTCTCATAGAGGTGAACCTG 6951
QY 61 GAGAGCGATCAGCAGAGCAATGTGACAAATGACCCCGAGGCACTCTCAGCCGAGCTG 120
Db 6952 GAGAGCGATCAGCAGAGCAATGTGACAAATGACCCCGAGGCACTCTCAGCCGAGCTG 7011
QY 121 GTGCCATCACTCTGCTGCTGTTTGTGATCGGTGTCCTGGACAACTCTCCTGGTTGTG 180
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RESULT 8

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US-10-029-386-22780
; Sequence 22780, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
```

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Db 7012 GTGCCATCACTCTGCTCTGCTGTTGTGATCGGTGTCTCGACAACTCTCCTGGTTGTG 7071
QY 181 CTTATCTCGGTAAAATATAAAGSACTCAAAACGGGTGGAATAATCTATCTTCTTAAACTTG 240
Db 7072 CTTATCTCGGTAAAATATAAAGSACTCAAAACGGGTGGAATAATCTATCTTCTTAAACTTG 7131
QY 241 GCAGTTTCTAACTGTGTTTCTTGTTCCTTACCTGCTCCCTCTATCTGGGCTCATGCTGGGGCGAT 300
Db 7132 GCAGTTTCTAACTGTGTTTCTTGTTCCTTACCTGCTCCCTCTATCTGGGCTCATGCTGRRGGCAT 7191
QY 301 CCCATGTGAAAATTTCTATTGGACTGTACTTCTGGGGGCTGTACAGTGAGACATTTTTC 360
Db 7192 CCCATGTGAAAATTTCTATTGGACTGTACTTCTGGGGGCTGTACAGTGAGACATTTTTC 7251
QY 361 AATTGCTCTCTGACTGTGCAAGGTACCTAGTGTGTTTGTGCAAGGGCAACTTTTCTCA 420
Db 7252 AATTGCTCTCTGACTGTGCAAGGTACCTAGTGTGTTTGTGCAAGGGCAACTTTTCTCA 7311
QY 421 GCCAGGAGGAGGTGCCCTGTGSCATCATTAAGGTGCTCTGGCATGGGTAAACAGCATT 480
Db 7312 GCCAGGAGGAGGTGCCCTGTGSCATCATTAAGGTGCTCTGGCATGGGTAAACAGCATT 7371
QY 481 CTGGCCACTTTGCCTGAATTCGTGGTTTATAAACTCAGATGGAAGACAGAAATACAAG 540
Db 7372 CTGGCCACTTTGCCTGAATTCWRTGGTTTATAAACTCAGATGGAAGACAGAAATACAAG 7431
QY 541 TGTGCATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTCCTGGAAGCATTTTCTG 600
Db 7432 TGTGCATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTCCTGGAAGCATTTTCTG 7491
QY 601 ACTTTAAATAATGAACATTTTCGGTTCCTGCTCCCTCTATTTATTTTACATTTCTCTAT 660
Db 7492 ACTTTAAATAATGAACATTTTCGGTTCCTGCTCCCTCTATTTATTTTACATTTCTCTAT 7551
QY 661 GTGCAAAATGAGAAAAACACTAAAGTTTCAGGGAGCAGAGGTATAGCCCTTTTCAAGCTTGT 720
Db 7552 GTGCAAAATGAGAAAAACACTAAAGTTTCAGGGAGCAGAGGTATAGCCCTTTTCAAGCTTGT 7611
QY 721 TTTGGCGTAATGGTAGTCTTCTCTGATGTTGGGCGCCCTACAAATATTTGCAATTTTCCCTG 780
Db 7612 TTTGGCGTAATGGTAGTCTTCTCTGATGTTGGGCGCCCTACAAATATTTGCAATTTTCCCTG 7671
QY 781 TCCACTTTCAAGAACACATTTCTCCCTGAGTGACTGCAAGAGCAGCTACAACTCTGGACAA 840
Db 7672 TCCACTTTCAAGAACACATTTCTCCCTGAGTGACTGCAAGAGCAGCTACAACTCTGGACAA 7731
QY 841 AGTGTTCACATCACTAAACTCATGCGCCACCACTGCTGCATCAACCCCTCTCCTGTAT 900
Db 7732 AGTGTTCACATCACTAAACTCATGCGCCACCACTGCTGCATCAACCCCTCTCCTGTAT 7791
QY 901 GCGTTTCTTGATGGGACATTTAGCAATACCTCTGCGCTGTTTCCATCTGCGTAGTAAC 960
Db 7792 GCGTTTCTTGATGGGACATTTAGCAATACCTCTGCGCTGTTTCCATCTGCGTAGTAAC 7851
QY 961 ACCCCACTTCAACCCAGGGGGAGTCTGCAAGGACACATCGAGGGAAGAACCTTGACCAT 1020
Db 7852 ACCCCACTTCAACCCAGGGGGAGTCTGCAAGGACACATCGAGGGAAGAACCTTGACCAT 7911
QY 1021 TCCACCGAAGTGTA 1035
Db 7912 TCCACCGAAGTGTA 7956
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; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AECOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 22780
; LENGTH: 1140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO U95626.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.99
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
; OTHER INFORMATION: EST_HUMAN HIT: B1834559.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: O97883, EVALUE 2.00e-63
; OTHER INFORMATION: NT HIT: G114736672, EVALUE 0.00e+00
US-10-029-386-22780

Query Match 99.7%; Score 1031.8; DB 16; Length 1140;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGCCCAATTACACGCTGGCACCAGAGGATGAATATGATGTCCTCATAGAGGTGAAGCTG 60
Db |
Qy 13 ATGCCCAATTACACGCTGGCACCAGAGGATGAATATGATGTCCTCATAGAGGTGAAGCTG 72
Db |
Qy 61 GAGAGCGATGAGGAGAGCAATGTGCAAGTATGACGCCAGGCACTCTCAGGCCAGCTG 120
Db |
Qy 73 GAGAGCGATGAGGAGAGCAATGTGCAAGTATGACGCCAGGCACTCTCAGGCCAGCTG 132
Db |
Qy 121 GTGCCATCACTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db |
Qy 133 GTGCCATCACTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 192
Db |
Qy 181 CTTATCTCGTAAATATAAGGACTCAACGCGTGGAAATATCTATCTCTAAAGCTG 240
Db |
Qy 193 CTTATCTCGTAAATATAAGGACTCAACGCGTGGAAATATCTATCTCTAAAGCTG 252
Db |
Qy 241 GCAGTTTCTAATCTGTTCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db |
Qy 253 GCAGTTTCTAATCTGTTCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 312
Db |
Qy 301 CCCATGTAAATCTCATGAGTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db |
Qy 313 CCCATGTAAATCTCATGAGTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 372
Db |
Qy 361 AATTGCTTCTGACTGTGCAAGGTACTACTGTGTTTTTGACAAGGGCAACTTTTCTCA 420
Db |
Qy 373 AATTGCTTCTGACTGTGCAAGGTACTACTGTGTTTTTGACAAGGGCAACTTTTCTCA 432
Db |
Qy 421 GCCAGGAGGAGGTCCTCTGTGGCATCATTAACAAGTCTCTGCGTCATGCGTAACAGCCATT 480
Db |
Qy 433 GCCAGGAGGAGGTCCTCTGTGGCATCATTAACAAGTCTCTGCGTCATGCGTAACAGCCATT 492
Db |
Qy 481 CTGCCCACTTGTCTGAAATCTGTTGTTTATAAATCTCAGATGGAGACCAAGATACAAAG 540
Db |
Qy 493 CTGCCCACTTGTCTGAAATCTGTTGTTTATAAATCTCAGATGGAGACCAAGATACAAAG 552
Db |
Qy 541 TGTCAATTTAGCAAGCTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db |
Qy 553 TGTCAATTTAGCAAGCTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 612
Db |
Qy 601 ACTTTAAATAATGAACATTTTGGTTTCTGCTCTCCCTCTATTTATTTTACATTTTCTCTAT 660
Db |
Qy 613 ACTTTAAATAATGAACATTTTGGTTTCTGCTCTCCCTCTATTTATTTTACATTTTCTCTAT 672
Db |
Qy 661 GTGCAATATGAAAAACACATTAAGTTTCAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 720
Db |
Qy 673 GTGCAATATGAAAAACACATTAAGTTTCAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 732
Db |

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: F3295P1C10
; CURRENT APPLICATION NUMBER: US/10/223,085
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383

RESULT 9
US-10-223-085-15
; Sequence 15, Application US/10223085
; Publication No. US20030100497A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Hurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: F3295P1C10
; CURRENT APPLICATION NUMBER: US/10/223,085
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383

721 TTGCGCCGTAATGGTAGTCTTCTTCTGATGGGGCCCTACAAATATTGCAATTTTCTG 780
733 TTGCGCATATGGTAGTCTTCTTCTGATGGGGCCCTACAAATATTGCAATTTTCTG 792
781 TCACATTTCAAGAACACTTCTCCTGAGTGATGCGAAGAGCAGCTACAAATCTGGACAAA 840
793 TCCACTTTCAAGAACACTTCTCCTGAGTGACTGCAAGAGCAGCTACAAATCTGGACAAA 852
841 AGTGTTCCACATCACTAACTCATGCGCCACCACCCACTGCTGCATCAACCCCTCTCTGTAT 900
853 AGTGTTCCACATCACTAACTCATGCGCCACCACCCACTGCTGCATCAACCCCTCTCTGTAT 912
901 GCGTTCCTTCTGATGGGACATTTAGCAAAATACCTCTGCGCGCTGTTTCCATCTGCGTAGTAAC 960
913 GCGTTCCTTCTGATGGGACATTTAGCAAAATACCTCTGCGCGCTGTTTCCATCTGCGTAGTAAC 972
961 ACCCACTTCAACCCAGGGGGGAGTCTGCAAGAGGACATCGAGGGAAGAACCTTGACCAT 1020
973 ACCCACTTCAACCCAGGGGGGAGTCTGCAAGAGGACATCGAGGGAAGAACCTTGACCAT 1032
1021 TCCACCGAAGTGTA 1035
1033 TCCACCGAAGTGTA 1047
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; SEQ ID NO 15									
; LENGTH: 1475									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-10-223-085-15									
Query Match 99.7%; Score 1031.8; DB 15; Length 1475;									
Best Local Similarity 99.8%; Pred. No. 0;									
Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY	1	ATGGCCAATTACAGCTGGCACCAGAGGATGAATATGATGCTCTCATAGAGGTGAAC	60						
DB	29	ATGGCCAATTACAGCTGGCACCAGAGGATGAATATGATGCTCTCATAGAGGTGAAC	88						
QY	61	GAGAGCGATGAGGAGAGCAATGTGACAAGTATGACGCCAGGCACCTCTCAGCCAGCTG	120						
DB	89	GAGAGCGATGAGGAGAGCAATGTGACAAGTATGACGCCAGGCACCTCTCAGCCAGCTG	148						
QY	121	GTCCCATCACTCTGCTCTGCTGTTTGTGATCGGTGCTCTGGACAATCTCCTGGTTGTG	180						
DB	149	GTCCCATCACTCTGCTCTGCTGTTTGTGATCGGTGCTCTGGACAATCTCCTGGTTGTG	208						
QY	181	CTTATCTCGTAAATATAAAGGACTCAACGGGTGGAAATATCTATCTTTAAACTTG	240						
DB	209	CTTATCTCGTAAATATAAAGGACTCAACGGGTGGAAATATCTATCTTTAAACTTG	268						
QY	241	GCAGTTTCTAACTTGTGTTCTTGTACCTGCGCTTCTGGGCTCATGCTGGGGCGAT	300						
DB	269	GCAGTTTCTAACTTGTGTTCTTGTACCTGCGCTTCTGGGCTCATGCTGGGGCGAT	328						
QY	301	CCCATGTGAAAATTCATTGAGCTGTACTTCTGGGCGCTGTACAGTGAGACATTTTTC	360						
DB	329	CCCATGTGAAAATTCATTGAGCTGTACTTCTGGGCGCTGTACAGTGAGACATTTTTC	388						
QY	361	AATTGCCCTCTGACTGTGCAAGGTACTAGTGTGTTTGGCAAGGGCAACTTTTCTCA	420						
DB	389	AATTGCCCTCTGACTGTGCAAGGTACTAGTGTGTTTGGCAAGGGCAACTTTTCTCA	448						
QY	421	GCAGAGGAGGGTGCCTGTGGCATCATTAACAAGTGTCTGGCATGGGTAAACAGCCATT	480						
DB	449	GCAGAGGAGGGTGCCTGTGGCATCATTAACAAGTGTCTGGCATGGGTAAACAGCCATT	508						
QY	481	CTGCCCATTTGCTGAATTCGTGTTTATAAACCCTCAGATGGAAGCAGCAATCAAG	540						
DB	509	CTGCCCATTTGCTGAATTCGTGTTTATAAACCCTCAGATGGAAGCAGCAATCAAG	568						
QY	541	TGTGCATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTTCTGGAAGCATTTCTG	600						
DB	569	TGTGCATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTTCTGGAAGCATTTCTG	628						
QY	601	ACTTTAAAAATGAACATTTTCGGTTCTTGTCCTCCCTCTATTTATTTTACATTTCTCTAT	660						
DB	629	ACTTTAAAAATGAACATTTTCGGTTCTTGTCCTCCCTCTATTTATTTTACATTTCTCTAT	688						
QY	661	GTCAAAATGAAAAACACTAAAGTTTCAGGAGCAGAGGTATAGCCCTTTTCAAGCTTGT	720						
DB	689	GTCAAAATGAAAAACACTAAAGTTTCAGGAGCAGAGGTATAGCCCTTTTCAAGCTTGT	748						
QY	721	TTTGGCGTAAATGGTAGTCTTCTCTTCTGATGTGGGCGCCCTACAAATATTGCAATTTTCTCTG	780						
DB	749	TTTGGCGTAAATGGTAGTCTTCTCTTCTGATGTGGGCGCCCTACAAATATTGCAATTTTCTCTG	808						
QY	781	TCACATTTTCAAAGAACACTCTCTCCCTGAGTGACTGCAAGAGCAGCTACAAATCTGGACAA	840						
DB	809	TCACATTTTCAAAGAACACTCTCTCCCTGAGTGACTGCAAGAGCAGCTACAAATCTGGACAA	868						
QY	841	AGTGTTCACATCACTAAACTCATGCCACCACCTGCTGTCATCAACCTCTCTCTGTAT	900						
DB	869	AGTGTTCACATCACTAAACTCATGCCACCACCTGCTGTCATCAACCTCTCTCTGTAT	928						
QY	901	GCGTTCCTTGATGGACATTTAGCAAAATACCTCTGCGCGCTGTTTCCATCTCGTAGTAAC	960						
DB	929	GCGTTCCTTGATGGACATTTAGCAAAATACCTCTGCGCGCTGTTTCCATCTCGTAGTAAC	988						
RESULT 10									
US-10-223-084-15									
; Sequence 15, Application US/10223084									
; Publication No. US20030105011A1									
; GENERAL INFORMATION:									
; APPLICANT: Baker, Kevin P.									
; APPLICANT: Ferrara, Napoleone									
; APPLICANT: Gerber, Hanspeter									
; APPLICANT: Gerritsen, Mary E.									
; APPLICANT: Goddard, Audrey									
; APPLICANT: Godowski, Paul J.									
; APPLICANT: Gurney, Austin L.									
; APPLICANT: Hillan, Kenneth J.									
; APPLICANT: Marsters, Scott A.									
; APPLICANT: Pan, James									
; APPLICANT: Stephan, Jean-Philippe F.									
; APPLICANT: Watanabe, Colin K.									
; APPLICANT: Wood, William I.									
; APPLICANT: Williams, P. Mickey									
; APPLICANT: Ye, Weilan									
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND									
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS									
; FILE REFERENCE: P3235P1C5									
; CURRENT APPLICATION NUMBER: US/10/223,084									
; CURRENT FILING DATE: 2002-08-16									
; PRIOR APPLICATION NUMBER: US 10/081,056									
; PRIOR FILING DATE: 2002-02-20									
; PRIOR APPLICATION NUMBER: US 60/213,637									
; PRIOR FILING DATE: 2000-06-23									
; PRIOR APPLICATION NUMBER: US 60/219,556									
; PRIOR FILING DATE: 2000-07-20									
; PRIOR APPLICATION NUMBER: US 60/220,624									
; PRIOR FILING DATE: 2000-07-25									
; PRIOR APPLICATION NUMBER: US 60/220,664									
; PRIOR FILING DATE: 2000-07-25									
; PRIOR APPLICATION NUMBER: PCT/US00/20710									
; PRIOR FILING DATE: 2000-07-28									
; PRIOR APPLICATION NUMBER: US 60/222,695									
; PRIOR FILING DATE: 2000-08-02									
; PRIOR APPLICATION NUMBER: US 09/643,657									
; PRIOR FILING DATE: 2000-08-17									
; PRIOR APPLICATION NUMBER: PCT/US00/23522									
; PRIOR FILING DATE: 2000-08-23									
; PRIOR APPLICATION NUMBER: PCT/US00/23328									
; PRIOR FILING DATE: 2000-08-24									
; Remaining Prior Application data removed - See File Wrapper or PALM.									
; NUMBER OF SEQ ID NOS: 383									
; SEQ ID NO 15									
; LENGTH: 1475									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-10-223-084-15									
Query Match 99.7%; Score 1031.8; DB 15; Length 1475;									
Best Local Similarity 99.8%; Pred. No. 0;									
Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY	1	ATGGCCAATTACAGCTGGCACCAGAGGATGAATATGATGCTCTCATAGAGGTGAAC	60						
DB	29	ATGGCCAATTACAGCTGGCACCAGAGGATGAATATGATGCTCTCATAGAGGTGAAC	88						
QY	61	GAGAGCGATGAGGAGAGCAATGTGACAAGTATGACGCCAGGCACCTCTCAGCCAGCTG	120						
DB	89	GAGAGCGATGAGGAGAGCAATGTGACAAGTATGACGCCAGGCACCTCTCAGCCAGCTG	148						
QY	121	GTCCCATCACTCTGCTCTGCTGTTTGTGATCGGTGCTCTGGACAATCTCCTGGTTGTG	180						
DB	149	GTCCCATCACTCTGCTCTGCTGTTTGTGATCGGTGCTCTGGACAATCTCCTGGTTGTG	208						
QY	181	CTTATCTCGTAAATATAAAGGACTCAACGGGTGGAAATATCTATCTTTAAACTTG	240						
DB	209	CTTATCTCGTAAATATAAAGGACTCAACGGGTGGAAATATCTATCTTTAAACTTG	268						
QY	241	GCAGTTTCTAACTTGTGTTCTTGTACCTGCGCTTCTGGGCTCATGCTGGGGCGAT	300						
DB	269	GCAGTTTCTAACTTGTGTTCTTGTACCTGCGCTTCTGGGCTCATGCTGGGGCGAT	328						
QY	301	CCCATGTGAAAATTCATTGAGCTGTACTTCTGGGCGCTGTACAGTGAGACATTTTTC	360						
DB	329	CCCATGTGAAAATTCATTGAGCTGTACTTCTGGGCGCTGTACAGTGAGACATTTTTC	388						
QY	361	AATTGCCCTCTGACTGTGCAAGGTACTAGTGTGTTTGGCAAGGGCAACTTTTCTCA	420						
DB	389	AATTGCCCTCTGACTGTGCAAGGTACTAGTGTGTTTGGCAAGGGCAACTTTTCTCA	448						
QY	421	GCAGAGGAGGGTGCCTGTGGCATCATTAACAAGTGTCTGGCATGGGTAAACAGCCATT	480						
DB	449	GCAGAGGAGGGTGCCTGTGGCATCATTAACAAGTGTCTGGCATGGGTAAACAGCCATT	508						
QY	481	CTGCCCATTTGCTGAATTCGTGTTTATAAACCCTCAGATGGAAGCAGCAATCAAG	540						
DB	509	CTGCCCATTTGCTGAATTCGTGTTTATAAACCCTCAGATGGAAGCAGCAATCAAG	568						
QY	541	TGTGCATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTTCTGGAAGCATTTCTG	600						
DB	569	TGTGCATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTTCTGGAAGCATTTCTG	628						
QY	601	ACTTTAAAAATGAACATTTTCGGTTCTTGTCCTCCCTCTATTTATTTTACATTTCTCTAT	660						
DB	629	ACTTTAAAAATGAACATTTTCGGTTCTTGTCCTCCCTCTATTTATTTTACATTTCTCTAT	688						
QY	661	GTCAAAATGAAAAACACTAAAGTTTCAGGAGCAGAGGTATAGCCCTTTTCAAGCTTGT	720						
DB	689	GTCAAAATGAAAAACACTAAAGTTTCAGGAGCAGAGGTATAGCCCTTTTCAAGCTTGT	748						
QY	721	TTTGGCGTAAATGGTAGTCTTCTCTTCTGATGTGGGCGCCCTACAAATATTGCAATTTTCTCTG	780						
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QY	781	TCACATTTTCAAAGAACACTCTCTCCCTGAGTGACTGCAAGAGCAGCTACAAATCTGGACAA	840						
DB	809	TCACATTTTCAAAGAACACTCTCTCCCTGAGTGACTGCAAGAGCAGCTACAAATCTGGACAA	868						
QY	841	AGTGTTCACATCACTAAACTCATGCCACCACCTGCTGTCATCAACCTCTCTCTGTAT	900						
DB	869	AGTGTTCACATCACTAAACTCATGCCACCACCTGCTGTCATCAACCTCTCTCTGTAT	928						
QY	901	GCGTTCCTTGATGGACATTTAGCAAAATACCTCTGCGCGCTGTTTCCATCTCGTAGTAAC	960						
DB	929	GCGTTCCTTGATGGACATTTAGCAAAATACCTCTGCGCGCTGTTTCCATCTCGTAGTAAC	988						

89	GAGAGCGATGAGGAGAGCAATGTGACAAAGTATGACGCCCAAGGCACATCTCTACGCCACAGCTG	148
121	GTGCCATCACTCTGCTCTGCTGTGTGTGTGATCGGGTGTCTCTGGACAATCTCTCTGTTGTG	180
149	GTGCCATCACTCTGCTCTGCTGTGTGTGTGATCGGTGTCTCTGGACAATCTCTCTGTTGTG	208
181	CTTATCTCGTGTAAATATAAAGGACTCAAAACCGCTGGAAATATCTATCTTCTAAACTTG	240
209	CTTATCTCGTGTAAATATAAAGGACTCAAAACCGCTGGAAATATCTATCTTCTAAACTTG	268
241	GCAGTTCTTAACCTGTGTTCTTGCTTTACCCCTGCCCCTCTGGGCTCATGCTGGGGCGAT	300
269	GCAGTTCTTAACCTGTGTTCTTGCTTTACCCCTGCCCCTCTGGGCTCATGCTGGGGCGAT	328
301	CCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGTGGCCCTGTACAGTGAGACATTTTTC	360
329	CCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGTGGCCCTGTACAGTGAGACATTTTTC	388
361	AATTGCCCTTCTGACTGTGCAAAGGTACTAGTGTGTTTTTGCACAAGGGCACTTTTCTCA	420
389	AATTGCCCTTCTGACTGTGCAAAGGTACTAGTGTGTTTTTGCACAAGGGCACTTTTCTCA	448
421	GCCAGGAGGAGGGTCCCTGTGGGCATCAATTACAAGTGTCTTGGCATGGGTAAACGCCATT	480
449	GCCAGGAGGAGGGTCCCTGTGGGCATCAATTACAAGTGTCTTGGCATGGGTAAACGCCATT	508
481	CTGSCCACTTTGCTCGTAATTCGTGGTTTATAAACCTCAGATGGAGAACCAGAAATACAAG	540
509	CTGSCCACTTTGCTCGTAATTCGTGGTTTATAAACCTCAGATGGAGAACCAGAAATACAAG	568
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569	TGTGCATTTAGCAGAACTCCCTTCTGCGCAGCTGATGAGACATTTCTGGAAGCATTTTCTG	628
601	ACTTTAAAAATGAACATTTGCGTTTCTGTCTCTCCCTCATTTATTTTACAATTTCTCTAT	660
629	ACTTTAAAAATGAACATTTGCGTTTCTGTCTCTCCCTCATTTATTTTACAATTTCTCTAT	688
661	GTGCAAAATGAGAAAAACACTAAGGTTCAGGGAGCAGAGGTATAGCCCTTTTCAAGCTTGT	720
689	GTGCAAAATGAGAAAAACACTAAGGTTCAGGGAGCAGAGGTATAGCCCTTTTCAAGCTTGT	748
721	TTTGGCCGTAATGGTAGTCTTCCCTCTCATGTGGGGCCCTACATATTGATTTTCTCCTG	780
749	TTTGGCCGTAATGGTAGTCTTCCCTCTCATGTGGGGCCCTACATATTTGCAATTTTCTCCTG	808
781	TCCACTTTTCAAGAAACAACCTTCTCCCTGAGTGACTGCAAGAGCAGCTACAATCTGACAAA	840
809	TCCACTTTTCAAGAAACAACCTTCTCCCTGAGTGACTGCAAGAGCAGCTACAATCTGACAAA	868
841	AGTGTTTCACATCACTAAACTCATCGCCAACAACCTGTCATCAACCCCTCTCCTGTAT	900
869	AGTGTTTCACATCACTAAACTCATCGCCAACAACCTGTCATCAACCCCTCTCCTGTAT	928
901	GGGTTTCTTGATGGGACATTTAGCAATACCTCTGCGCTGTTTCCATCTGCGTAGTAAC	960
929	GGGTTTCTTGATGGGACATTTAGCAATACCTCTGCGCTGTTTCCATCTGCGTAGTAAC	988
961	ACCCCACTTCAACCCAGGGGCGAGTCTGCAACAAGGCACATCGAGGGGAAGAACCTGACCAT	1020
989	ACCCCACTTCAACCCAGGGGCGAGTCTGCAACAAGGCACATCGAGGGGAAGAACCTGACCAT	1048
1021	TCCACCGAAGTGTA	1035
1049	TCCACCGAAGTGTA	1063

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; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Wickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C6
; CURRENT APPLICATION NUMBER: US/10/223,088
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-223-088-15

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RESULT 11
US-10-223-088-15
; Sequence 15, Application US/10223088
; Publication NO. US20030105012A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

Db 329 CCATGTGTAATAATTCATTGGACTGTACTTCTGGGCGCTGTACAGTGAGACATTTTTC 388
Qy 361 AATTGCTTCTGACTGTGCAAGGTACCTAGTGTGTTTGCAAGGGCACTTTTCTCA 420
Db 389 AATTGCTTCTGACTGTGCAAGGTACCTAGTGTGTTTGCAAGGGCACTTTTCTCA 448
Qy 421 GCAGAGAGAGGGTGCCCTGTGGCATCATTAACAAGTGTCTCGCATGGGTAACAGCCATT 480
Db 449 GCAGAGAGAGGGTGCCCTGTGGCATCATTAACAAGTGTCTCGCATGGGTAACAGCCATT 508
Qy 481 CTGGCCACTTTGGCTGAATTCGTGGTTTATAAACCCTCAGATGGAAGACCAAGAAATCAAG 540
Db 509 CTGGCCACTTTGGCTGAATTCGTGGTTTATAAACCCTCAGATGGAAGACCAAGAAATCAAG 568
Qy 541 TGTGCATTAGCAGAACTCCCTTCTGCGAGCTGTAGACATCTGGAAGCAATTTCTG 600
Db 569 TGTGCATTAGCAGAACTCCCTTCTGCGAGCTGTAGACATCTGGAAGCAATTTCTG 628
Qy 601 ACTTTAAAAATGAACATTTCCGTTCTTGTCTCTCCCTATTTATTTTACATTTCTCTAT 660
Db 629 ACTTTAAAAATGAACATTTCCGTTCTTGTCTCTCCCTATTTATTTTACATTTCTCTAT 688
Qy 661 GTCAATATGAAGAAACACATTAAGTTTCAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 720
Db 689 GTCAATATGAAGAAACACATTAAGTTTCAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 748
Qy 721 TTTGCCGTATAGTACTTCTTCTGATGTGGCGCCCTACAAATTTGCAATTTTCCCTG 780
Db 749 TTTGCCGTATAGTACTTCTTCTGATGTGGCGCCCTACAAATTTGCAATTTTCCCTG 808
Qy 781 TCCACTTTCAAGAAACACTTCTCCCTGAGTACTGCAAGAGCAGCTACAACTCTGGACAA 840
Db 809 TCCACTTTCAAGAAACACTTCTCCCTGAGTACTGCAAGAGCAGCTACAACTCTGGACAA 868
Qy 841 AGTGTTCACATCACTAACTCATCGCCACCAACCACCTGTGTCATCAACCCCTCTCTGTAT 900
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Qy 901 GCCTTTCTGATGGGACATTTAGCAATACCTCTGCGCTGTTTCCATCTGCGTAGTAAC 960
Db 929 GCCTTTCTGATGGGACATTTAGCAATACCTCTGCGCTGTTTCCATCTGCGTAGTAAC 988
Qy 961 ACCCCACTTCAACCCAGGGGCGAGTCTGCACAAGGGCACATCGAGGGAAGAACCTGACCAT 1020
Db 989 ACCCCACTTCAACCCAGGGGCGAGTCTGCACAAGGGCACATCGAGGGAAGAACCTGACCAT 1048
Qy 1021 TCCACCGAAGTGTA 1035
Db 1049 TCCACCGAAGTGTA 1063

RESULT 12
US-10-223-090-15
; Sequence 15, Application US/10223090
; Publication No. US20030105013A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS

; FILE REFERENCE: P3235PIC2
; CURRENT APPLICATION NUMBER: US/10/223,090
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-223-090-15

Query Match 99.7%; Score 1031.8; DB 15; Length 1475;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ATGGCCAATTACACGCTGGCACAGAGGATGAATATGATGTCTCTCATAGAAGTGAACGTG 60
Db 29 ATGGCCAATTACACGCTGGCACAGAGGATGAATATGATGTCTCTCATAGAAGTGAACGTG 88
Qy 61 GAGAGCGATGAGGAGAGCAATGTGACAGTATGACCCAGGCACTCTCAGCCAGCTG 120
Db 89 GAGAGCGATGAGGAGAGCAATGTGACAGTATGACCCAGGCACTCTCAGCCAGCTG 148
Qy 121 GTGCCATCACTCTGCTCTGCTGTGTTGTGATCGGTGTCTGGACAATCTCTGTTGTG 180
Db 149 GTGCCATCACTCTGCTCTGCTGTGTTGTGATCGGTGTCTGGACAATCTCTGTTGTG 208
Qy 181 CTTATCCTGGTAAATATATAAGGACTCAAAACGCGTGGAAAAATATCTATCTTTAAACTTG 240
Db 209 CTTATCCTGGTAAATATATAAGGACTCAAAACGCGTGGAAAAATATCTATCTTTAAACTTG 268
Qy 241 GCAGTTTCTAACTGTGTTTCTTGCTTACCTGCCCTTCTGGGCTCATGCTGGGGCGAT 300
Db 269 GCAGTTTCTAACTGTGTTTCTTGCTTACCTGCCCTTCTGGGCTCATGCTGGGGCGAT 328
Qy 301 CCCATGTGTAATAATCTCTCACTGGACTGTACTCTGCGGCTGTACAGTGAGACATTTTTC 360
Db 329 CCCATGTGTAATAATCTCTCACTGGACTGTACTCTGCGGCTGTACAGTGAGACATTTTTC 388
Qy 361 AATTGCTTCTGACTGTGCAAGGTACCTAGTGTGTTTTCACAAGGGCAACTTTTCTCA 420
Db 389 AATTGCTTCTGACTGTGCAAGGTACCTAGTGTGTTTTCACAAGGGCAACTTTTCTCA 448
Qy 421 GCCAGAGAGGGTGCCCTGTGGCATCATTAACAAGTGTCTCGCATGGGTAACAGCCATT 480
Db 449 GCCAGAGAGGGTGCCCTGTGGCATCATTAACAAGTGTCTCGCATGGGTAACAGCCATT 508
Qy 481 CTGGCCACTTTGCTGCAATTCGTGGTTTATAAACCCTCAGATGGAAGACCAAGAAATCAAG 540
Db 509 CTGGCCACTTTGCTGCAATTCGTGGTTTATAAACCCTCAGATGGAAGACCAAGAAATCAAG 568
Qy 541 TGTGCATTAGCAGAACTCCCTTCTGCGAGCTGTAGACATCTGGAAGCAATTTCTG 600

Db 569 TGTGCAATTTAGCAGAACTCCCTTCTCGCCAGCTGATGAGACATTCGGAAGCAATTTCTG 628
Qy 601 ACTTTAAAAATGAACATTTTCGGTTCTTCTCTCCCTATTTATTTTACATTTCTCTAT 660
Db 629 ACTTTAAAAATGAACATTTTCGGTTCTTCTCTCCCTATTTATTTTACATTTCTCTAT 688
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Db 689 GTGCAATGAGAAAAACACTAAGTTTCAGGAGCAGAGGTATAGCCTTTTCAAGCTTGTT 748
Qy 721 TTGCGCGTAATGGTAGTCTTCTCTGATGTGGGCGCCCTACAATATTGCAATTTTCTG 780
Db 749 TTGCGCAATGAGTAGTCTTCTCTGATGTGGGCGCCCTACAATATTGCAATTTTCTG 808
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Qy 841 AGTGTTCACATCACTAACTCATGCGCACCAACCCTGCTGCATCAACCCCTCTCTGTAT 900
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Qy 901 CGGTTTCTTGATGGACATTTAGCAAAATACCTCTGCGCTGTTTCCATCTCGTAGTAAC 960
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Db 989 ACCCCTTTCAACCCAGGGGCGAGTCTGCACAAGGCACATCGAGGGAAGAACCTTGACCAT 1048
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RESULT 13

US-10-223-087-15
; Sequence 15, Application US/10223087
; Publication No. US20030109438A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235PlC4
; CURRENT APPLICATION NUMBER: US/10/223,087
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695

; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/230,978
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/232,887
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 09/664,610
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/242,922
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/709,238
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30952
; PRIOR FILING DATE: 2000-11-08
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; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/767,609
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 09/796,498
; PRIOR FILING DATE: 2001-02-28
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; PRIOR APPLICATION NUMBER: PCT/US01/06666
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; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/808,689
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 09/816,744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 09/828,366
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; PRIOR APPLICATION NUMBER: US 09/870,574
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; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-223-087-15

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Matches 1033;		Conservative	0;	Mismatches	2; Indels 0; Gaps 0;
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Db	149	GTGCGATCACTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	208		
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Qy	241	GCAGTTTCTAACTGTGTTTCTTGTCTTACCGTCCCTTCTGGGCTCATGCTGG	300		
Db	269	GCAGTTTCTAACTGTGTTTCTTGTCTTACCGTCCCTTCTGGGCTCATGCTGG	328		
Qy	301	CCCATGTGTAATAATCTCATTTGACTGTACTTCTGCGGCTGTACAGTGAGACA	360		
Db	329	CCCATGTGTAATAATCTCATTTGACTGTACTTCTGCGGCTGTACAGTGAGACA	388		
Qy	361	AATTGCCCTCTGACTGTGCAAGGTACCTAGTGTGTTTTCACAAGGGCAACT	420		
Db	389	AATTGCCCTCTGACTGTGCAAGGTACCTAGTGTGTTTTCACAAGGGCAACT	448		
Qy	421	GCCAGGAGGAGGTGCGCTGTGCAATCATTAACAGTGTCTGCGATGGGTAA	480		
Db	449	GCCAGGAGGAGGTGCGCTGTGCAATCATTAACAGTGTCTGCGATGGGTAA	508		
Qy	481	CTGCCCACTTTGCTGAATTCGTGGTTTATAAACCTCAGATGAAGACAGAA	540		
Db	509	CTGCCCACTTTGCTGAATTCGTGGTTTATAAACCTCAGATGAAGACAGAA	568		
Qy	541	TGTGCATTTAGCAAACTCCCTTCTGCGAGCTGATGAGACATTTCTGGA	600		
Db	569	TGTGCATTTAGCAAACTCCCTTCTGCGAGCTGATGAGACATTTCTGGA	628		
Qy	601	ACTTTAAATGAACATTTTGGTTTCTGCTCCCTTATTTTATTTTACATTT	660		
Db	629	ACTTTAAATGAACATTTTGGTTTCTGCTCCCTTATTTTATTTTACATTT	688		
Qy	661	GTGCAATGAGAAAAACACTTAAGTTTCAGGAGCAGAGGTATAGCCTTTT	720		
Db	689	GTGCAATGAGAAAAACACTTAAGTTTCAGGAGCAGAGGTATAGCCTTTT	748		
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Db	749	TTTGGCGTAAATGTTAGTCTTCTTCTGATGCGGCGCTTACAAATATTG	808		
Qy	781	TCACATTTCAAGAACACTTCTCCCTGAGTACTGCAAGAGCAGCTACATCT	840		
Db	809	TCACATTTCAAGAACACTTCTCCCTGAGTACTGCAAGAGCAGCTACATCT	868		
Qy	841	AGTGTTCACATCACTAACTCATCGCCACCACTCATGCTGCAATCAACCT	900		
Db	869	AGTGTTCACATCACTAACTCATCGCCACCACTCATGCTGCAATCAACCT	928		
Qy	901	CGGTTTCTGATGGGCAATTTAGCAATACCTCTGCGGCTGTTTCCATCTG	960		
Db	929	CGGTTTCTGATGGGCAATTTAGCAATACCTCTGCGGCTGTTTCCATCTG	988		
Qy	961	ACCCCACTTCAACCCAGGGGGAGTCTGCAACAGGCACATCGAGGGAAG	1020		
Db	989	ACCCCACTTCAACCCAGGGGGAGTCTGCAACAGGCACATCGAGGGAAG	1048		

Qy	1021	TCCACCGAAGTGTAA	1035
Db	1049	TCCACCGAAGTGTAA	1063
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; Sequence 15, Application US/10223083			
; Publication No. US20030119112A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Ferrara, Napoleone			
; APPLICANT: Gerber, Hanspeter			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Hillan, Kenneth J.			
; APPLICANT: Marsters, Scott A.			
; APPLICANT: Pan, James			
; APPLICANT: Stephan, Jean-Philippe F.			
; APPLICANT: Watanabe, Colin K.			
; APPLICANT: Wood, William I.			
; APPLICANT: Williams, P.Mickey			
; APPLICANT: Ye, Weilan			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND			
; FILE REFERENCE: P3235PIC8			
; CURRENT APPLICATION NUMBER: US/10/223,083			
; CURRENT FILING DATE: 2002-08-16			
; PRIOR APPLICATION NUMBER: US 10/081,056			
; PRIOR FILING DATE: 2002-02-20			
; PRIOR APPLICATION NUMBER: US 60/213,637			
; PRIOR FILING DATE: 2000-06-23			
; PRIOR APPLICATION NUMBER: US 60/219,556			
; PRIOR FILING DATE: 2000-07-20			
; PRIOR APPLICATION NUMBER: US 60/220,624			
; PRIOR FILING DATE: 2000-07-25			
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; PRIOR FILING DATE: 2000-08-24			
; Remaining Prior Application data removed - See File Wrapper or PALM.			
; NUMBER OF SEQ ID NOS: 383			
; SEQ ID NO 15			
; LENGTH: 1475			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-223-083-15			

Query Match 99.7%; Score 1031.8; DB 15; Length 1475;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ATGGCCAAATTACACGCTGGCAGGAGTGAATATGATGTCTCTCATAGAGGTGAAC	60
Db	29	ATGGCCAAATTACACGCTGGCAGGAGTGAATATGATGTCTCTCATAGAGGTGAAC	88
Qy	61	GAGAGCGATGAGGAGAGCAATGTGACAAGTATGACGCCCGAGGCACTCTCAGCC	120
Db	89	GAGAGCGATGAGGAGAGCAATGTGACAAGTATGACGCCCGAGGCACTCTCAGCC	148
Qy	121	GTGCCATCACTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	180
Db	149	GTGCCATCACTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	208

Qy	421	GCAGGAGGAGGTGCCCTGTGGCATCATTTACAAGTGTCTCTGGCATGGGTAAACAGCCATT	480
Db	449	GCAGGAGGAGGTTGCCCTGTGGCATCATTTACAAGTGTCTCTGGCATGGGTAAACAGCCATT	508
Qy	481	CTGGCCACTTTTGCTCGTGAATTCGTGGTTTATAAACCCTCAGATGGAAGACCAAGAAATACAAG	540
Db	509	CTGGCCACTTTTGCTCGTGAATTCGTGGTTTATAAACCCTCAGATGGAAGACCAAGAAATACAAG	568
Qy	541	TGTGCATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACATTTCTGGAAGCAATTTTCTG	600
Db	569	TGTGCATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACATTTCTGGAAGCAATTTTCTG	628
Qy	601	ACTTTAAATAATGAACATTTTCGGTTCTTGTCTCTCCCTATTTATTTTACATTTCTCTAT	660
Db	629	ACTTTAAATAATGAACATTTTCGGTTCTTGTCTCTCCCTATTTATTTTACATTTCTCTAT	688
Qy	661	GTGCAATGAGAAAAACACTAAGGTTTCAGGGAGCAGAGGTATAGCCCTTTTCAAGCTTGT	720
Db	689	GTGCAATGAGAAAAACACTAAGGTTTCAGGGAGCAGAGGTATAGCCCTTTTCAAGCTTGT	748
Qy	721	TTTGCGGTAAATGTAGTCTTCTCTGTGATGTGGGCGCCCTACAAATATTGCAATTTTCTCTG	780
Db	749	TTTGCGGTAAATGTAGTCTTCTCTGTGATGTGGGCGCCCTACAAATATTGCAATTTTCTCTG	808
Qy	781	TCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTACAAATCTGGACAAA	840
Db	809	TCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTACAAATCTGGACAAA	868
Qy	841	AGTGTTCACATCACTAAACTCATCGCCACCACTGCTGTCATCAACCCCTCTCTGTAT	900
Db	869	AGTGTTCACATCACTAAACTCATCGCCACCACTGCTGTCATCAACCCCTCTCTGTAT	928
Qy	901	CGGTTTCTTGATGGGACATTTAGCAATACCTCTGCGGCTGTTTCCATCTGCGTAGTAAC	960
Db	929	CGGTTTCTTGATGGGACATTTAGCAATACCTCTGCGGCTGTTTCCATCTGCGTAGTAAC	988
Qy	961	ACCCCACTTCAACCCAGGGGCGAGTCTGCACAAGGCACATCGAGGGGAAGAACCTGACCAT	1020
Db	989	ACCCCACTTCAACCCAGGGGCGAGTCTGCACAAGGCACATCGAGGGGAAGAACCTGACCAT	1048
Qy	1021	TCCACCGAAGTGTA 1035	
Db	1049	TCCACCGAAGTGTA 1063	

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Job time : 728.252 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 18, 2005, 06:38:50 ; Search time 4139.74 Seconds
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9958.019 Million cell updates/sec

Title: US-10-623-472-32

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: gb_est1.*

2: gb_est2.*

3: gb_hcc.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gse1.*

9: gb_gse2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	770.6	71.2	885	4 BI082667	BI082667 602878081
3	664.2	61.3	958	4 BI408316	BI408316 602962210
4	604.6	55.8	770	7 CV118408	CV118408 AGENCOURT
5	585.8	54.1	810	2 BE911886	BE911886 601662628
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8	529	48.8	540	4 BM247265	BM247265 K0749D08-
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ACCESSION AK007808
VERSION AK007808.1 GI:12841594
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SOURCE Mus musculus
ORGANISM Mus musculus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636

REFERENCE 2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitagawa, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaehiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
MEDLINE 11076861
PUBMED 11076861
REFERENCE 5
The FANTOM Consortium and the RIKEN Genome Exploration Research


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SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 885)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 828.
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Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match 71.2%; Score 770.6; DB 4; Length 885;
Best Local Similarity 98.7%; Pred. No. 9e-215;
Matches 850; Conservative 0; Mismatches 4; Indels 7; Gaps 7;

Qy 136 GCGGTGTTGGGTGGGTCTCTGACAACTGCTGGCGGTTTATCTTGCTGAATAC 195
|||
Db 1 CGGTGTTGGGTGGGTCTCTGACAACTGCTGGCGGTTTATCTTGCTGAATAC 60
|||

Qy 196 AAAGGACTCAAGAACTCGGGGAACATCTACTTCTTAAACCTGGCACTTTCAAACCTGTGT 255
|||
Db 61 AAAGGACTCAAGAACTCGGGGAACATCTACTTCTTAAACCTGGCACTTTCAAACCTGTGT 120
|||

Qy 256 TTCTGCTTCCCTGCGGTTCTGGGCCCATACTGCGAGCACACGGGGAAGCCCTGGCAAC 315
|||
Db 121 TTCTGCTTCCCTGCGGTTCTGGGCCCATACTGCGAGCACACGGGGAAGCCCTGGCAAC 180
|||

Qy 316 GGGACCTGTAAGTCTTGTGGGACTCCACCTCCGCGCTTATACAGCGAGGTGTTTTCC 375
|||
Db 181 GGGACCTGTAAGTCTTGTGGGACTCCACCTCCGCGCTTATACAGCGAGGTGTTTTCC 240
|||

Qy 376 AACATCCTCCTCCTTGTGCAAGGATACAGGGTGTGTTTCCCAAGGCGCACTGGCCTCCATC 435
|||
```

```
Db 241 AACATCCTCCTCCTTGTGCAAGGATACAGGGTGTGTTTCCCAAGGCGCACTGGCCTCCATC 300
|||
Qy 436 TTACGACAGGTCTTGTGTTATTTGTCGTCATCTCGGCATCGGCATCGGCATCGGTACTGG 495
|||
Db 301 TTACGACAGGTCTTGTGTTATTTGTCGTCATCTCGGCATCGGCATCGGTACTGG 360
|||
Qy 496 CTCTCTTTGCCCGAGTCTGTGTTTTATGAGCCTCGATGGAAGACACAAACACAAAGTGT 555
|||
Db 361 CTCTCTTTGCCCGAGTCTGTGTTTTATGAGCCTCGATGGAAGACACAAACACAAAGTGT 420
|||
Qy 556 GCCTTTGGCAAACTCACTTCTTCCCAATCGAAGCGCGCTCTGGAAGTACGTTCTGAGG 615
|||
Db 421 GCCTTTGGCAAACTCACTTCTTCCCAATCGAAGCGCGCTCTGGAAGTACGTTCTGAGG 480
|||
Qy 616 TCRAAATGATCATCTTGGTACTTGTCTTCTCTGCTGGTTTTTATATATATGCTGCGAGG 675
|||
Db 481 TCRAAATGATCATCTTGGTACTTGTCTTCTCTGCTGGTTTTTATATATATGCTGCGAGG 540
|||
Qy 676 CAACCTGAGGGAAGCGCAGAGCTTCAGGAGAGACAGTACGACCTCCACAAGCGGCTCTT 735
|||
Db 541 CAACCTGAGGGAAGCGCAGAGCTTCAGGAGAGACAGTACGACCTCCACAAGCGGCTCTT 600
|||
Qy 736 GTCATAAACGGCGGTCTCTTTTGTATGTTGGCGCTTACAAACATCTGCTTTTCTGCTCT 795
|||
Db 601 GTCATAAACGGCGGTCTCTTTTGTATGTTGGCGCTTACAAACATCTGCTTTTCTGCTCT 660
|||
Qy 796 GCTTTCAGGGAACACTTGTCTCTCAGATCAGAGAGCAGTACCACTTGAGCGCAAGT 855
|||
Db 661 GCTTTCAGGGAACACTTGTCTCTCAGATCAGAGAGCAGTACCACTTGAGCGCAAGT 719
|||
Qy 856 GTTCAGGTTCACACAGCTGGTAGCAGCACCACTGCTGCTCAACCC-GCTGCTCTATT 914
|||
Db 720 G-TCAGGTTCACACAGCTGGTAGCAGTCAACCACTGCTGCTCAACCCGCTGCTCTATAT 778
|||
Qy 915 GC-TTCTTGACCGGAA-GGCCTTTATGAGTACCTT-CGAGCTGTTTCCCAAGTGCNA 971
|||
Db 779 GCTTCTTGACCGGAGGGCTTTATGAGTACCTTCCGCGACCTGTTTCCCAAGTGCNA 838
|||

Qy 972 TGATA-TCCCTCATCAAGTA 991
|||
Db 839 TGATATTCCCTCATCAAGTA 859
|||

RESULT 3
BI08316
LOCUS 602962210P1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5117522 5',
DEFINITION mRNA sequence.
ACCESSION BI08316
VERSION BI08316.1 GI:15169239
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 958)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11286 row: d column: 03
High quality sequence stop: 939.
```

Qy	711	GTACGACCTTCCA--CAAGCGGCTCTTGTCTATACAGCGGCGTGTTC--TTTGTATGTGGG	766
Db	871	GTACGACCTTCCAACAAAGCGGGTCTTGTCTATACAGCGGCGTGTTCCTTTTCGATGTGG	930
Qy	767	CGCCTT-ACAACACACTGTGCTTTTCC	790
Db	931	CGCCTTAAACACCTGTGCTTTTC	955
RESULT 4			
LOCUS CV116408			
DEFINITION Rattus norvegicus (Norway rat)			
ACCESSION CV116408			
VERSION CV116408.1 GI:51635215			
KEYWORDS EST.			
SOURCE Rattus norvegicus			
ORGANISM Rattus norvegicus			
REFERENCE 1 (bases 1 to 770)			
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.			
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL Unpublished (1999)			
COMMENT Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgabbs-remail.nih.gov Tissue Procurement: Dr. Josef Lazar, Dr. Howard J. Jacob, Medical College of Wisconsin CDNA Library Preparation: Open Biosystems CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM15745 row: j column: 16 High quality sequence stop: 713.			
FEATURES			
source			
1. 770			
/organism="Rattus norvegicus"			
/mol_type="mRNA"			
/db_xref="taxon:10116"			
/clone="IMAGE:7445010"			
/tissue_type="whole placenta, 2 pooled"			
/lab_host="DH10B Tona"			
/clone_lib="NIH MGC_270"			
/note="Organ: placenta; Vector: pExpress-1; Site 1: EcoRV; Site 2: NotI; Tissue was collected from two pooled placentas from the 21st day of pregnancy. 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was cloned into the Not I and EcoRV sites of pExpress-1. Library was size-selected for >1.25 kb fragments for an average insert size of 2.15 kb. Library was normalized to Cot7. A non-normalized version of this library is also available (NIH MGC 269). Library was constructed by Open Biosystems (Huntsville, AL). Note: this is a Mammalian Gene Collection library"			
ORIGIN			
Query Match 55.8%; Score 604.6; DB 7; Length 770;			
Best Local Similarity 88.0%; Pred. No. 5.4e-166;			
Matches 669; Conservative 0; Mismatches 90; Indels 1; Gaps 1;			
Qy	47	TCCTTAGCAGTACCTGGACACAGTGGCGGACCAAGTTCCGGCCCGGAGTTCCTCT	106
Db	4	TCATAGAGTATGACCTGGACACAGTGGCGGACCAAGTTCCACCCCGGAGTTCCTCT	63
Qy	107	CCCCCAGCAGGCTGTCAGATTTCTGTCGCGGTGTTTTCGCGGTGCTCTTGTGACACG	166


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CO425383
LOCUS      CO425383            801 bp      mRNA      linear      EST 06-JUL-2004
DEFINITION UI-M-HUO-cra-i-17-0-UI.r1 NIH_BMAP_HU0 Mus musculus cDNA clone
IMAGE:30670960 5', mRNA sequence.
ACCESSION  CO425383
VERSION     CO425383.1   GI:49671677
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 801)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-r@mail.nih.gov
              Tissue Procurement: Dr. James Lin University of Iowa
              cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
              DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
              Clone Distribution: Distribution Information can be found at
              http://genome.uiowa.edu/distribution/mousefl.html
              This clone was contributed by the Brain Molecular Anatomy Project
              (BMAP)
Seq primer: pyX-5.
Location/Qualifiers
1. .801
   /organism="Mus musculus"
   /mol_type="mRNA"
   /strain="C57BL/6"
   /db_xref="taxon:10090"
   /clone="IMAGE:30670960"
   /tissue_type="whole eye"
   /dev_stage="newborn (1, 5, 15 days)"
   /lab_host="DH10B (T1 phage resistant)"
   /clone_lib="NIH_BMAP_HU0"
   /notes="Organ: Eye; Vector: pyX-Asc; Site 1: Ecor I;
   Site 2: Not I; The library was constructed according
   Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
   1996. Denatured RNA was size fractionated on a 1% agarose
   gel. First strand cDNA synthesis was primed with oligo-dT
   primer containing a Not I site. Double strand cDNA was
   size selected according to mRNA size fraction, ligated
   with Ecor I adaptor, digested with NotI and then cloned
   directionally into pyX-Asc vector. The library tag
   sequence located between the Not I site and the polyA tail
   is AATAATTACG. This library was created for the University
   Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
   Developing Mouse Nervous System', supported by National
   Institute of Mental Health (NIMH)."
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ORIGIN

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Query Match      49.5%; Score 536.6; DB 7; Length 801;
Best Local Similarity 98.9%; Pred. No. 5.4e-146;
Matches 539; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY  1  ATGGATAACTACACAGTGGCCCCGGACGATGAATATGATCTCTTAATCTTAGACGACTAC 60
    |||
DB  246 ATGGATAACTACACAGTGGCCCCGGACGATGAATATGATCTCTTAATCTTAGACGACTAC 305
    |||

QY  61  CTGGACACAGTGGCGCGGACCAAGTTCCGCGCCCCCGAGTTCCTCTCCCCCGACGAGTG 120
    |||
DB  306 CTGGACACAGTGGCGCGGACCAAGTTCCGCGCCCCCGAGTTCCTCTCCCCCGACGAGTG 365
    |||

QY  121 CTGCAGTCTCTGCTGCGCGGTGTTTGGCGGTGGTCTCTTTGACACACGTCGTGGCGGTGTTT 180
    |||
DB  366 CTGCAGTCTCTGCTGCGCGGTGTTTGGCGGTGGTCTCTTTGACACACGTCGTGGCGGTGTTT 425
    |||

QY  181 ATCTTGTGTAATACAAAGAGCTCAAGAATCTGGGGGAACATCTACTTCTCTAAACCTGGCA 240
    |||
DB  426 ATCTTGTGTAATACAAAGAGCTCAAGAATCTGGGGGAACATCTACTTCTCTAAACCTGGCA 485
    |||
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QY  241 CTTTCAAACTGTGTTTCTGCTTCCCTGCGCTTCCCTGCGCTTCTGGGCCCATCTACTGCAGCACACGGG 300
    |||
DB  486 CTTTCAAACTGTGTTTCTGCTTCCCTGCGCTTCCCTGCGCTTCTGGGCCCATCTACTGCAGCACACGGG 545
    |||

QY  301 GAAAGCCCTGGCAACCGGACCTGTAAAGTTCTTGTGCGGACTCCCTCGGCTTTATAC 360
    |||
DB  546 GAAAGCCCTGGCAATGGGACCTGTAAAGTTCTTGTGCGGACTCCCTCGGCTTTATAC 605
    |||

QY  361 AGCGAGGTGTTTCCCAACATCCCTCCCTGTCGCAAGGATACAGGCTGTTTCCCAAGGG 420
    |||
DB  606 AGCGAGGTGTTTCCCAACATCCCTCCCTGTCGCAAGGATACAGGCTGTTTCCCAAGGG 665
    |||

QY  421 CGACTGGCCTCCATCTTTCACGACAGTGTCTTGTGGTATTGTTGCGTGCATCTCGGCATGG 480
    |||
DB  666 CGACTGGCCTCCATCTTTCACGACAGTGTCTTGTGGTATTGTTGCGTGCATCTCGGCATGG 725
    |||

QY  481 GCCATGGCTACTGCGCTCTCTTTGCGGAGTCTGTGTTTATGAGCCTCGGATGGAAAGA 540
    |||
DB  726 GCCATGGCTACTGCGCTCTCTTTTGGCGAGTCTGTGTTTATGAGCCTCGGATGGAAAGA 785
    |||

QY  541 CAGAA 545
    |||
DB  786 CAGAA 790
    |||

RESULT 7
LOCUS      BG863198
DEFINITION 602796680F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4917762 5',
mRNA sequence.
ACCESSION  BG863198
VERSION     BG863198.1   GI:14213736
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 700)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-r@mail.nih.gov
              Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
              Ph.D.
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone Distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: L1AM10829 row: p column: 19
              High quality sequence stop: 700.
              Location/Qualifiers
1. .700
   /organism="Mus musculus"
   /mol_type="mRNA"
   /strain="NMRI"
   /db_xref="taxon:10090"
   /clone="IMAGE:4917762"
   /tissue_type="tumor, gross tissue"
   /dev_stage="5 months"
   /lab_host="DH10B"
   /clone_lib="NCI_CGAP_Mam4"
   /notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
   Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
   Library constructed by Life Technologies. Investigators
   providing samples: Lothar Hennighausen/Priscilla Furth,
   NIH Reference for transgenic model: Li et al., Cell Growth
   and Differentiation 7, 3-11 (1996)."
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ORIGIN

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Query Match      49.4%; Score 535.4; DB 4; Length 700;
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Db      120  TATCCCTATCAAGTAGTGGAGGCTATCAGCAAGCGCTCCCAAGGAGGTATGCGCAG 61
Qy      1035 GCCATTGAACTGTACAGCAATTTGCAATCAAGCGCAGGATATATATAA 1083
Db      60  GCCATTGAACTGTACAGCAATTTGCAATCAAGCGCAGGATATATATAA 12

RESULT 9
CK839171/c
LOCUS      721 bp      mRNA      linear      EST 05-MAR-2004
DEFINITION UI-R-AA1-zw-f-06-0-UI-s10 UI-R-AA1 Rattus norvegicus cDNA clone
            UI-R-AA1-zw-f-06-0-UI 3', mRNA sequence.
ACCESSION  CK839171
VERSION     CK839171.1 GI:45189928
KEYWORDS   EST.
SOURCE     Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE  1 (bases 1 to 721)
            Bonaudo,M.F., Lennon,G. and Soares,M.B.
            Normalization and subtraction: two approaches to facilitate gene
            discovery
            Genome Res. 6 (9), 791-806 (1996)
JOURNAL    97044477
MEDLINE    8889548
PubMed     8889548
COMMENT    Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/rat.html
            The following repetitive elements were found in this cDNA
            sequence: 1-37, >POLY A#Simple_repeat (matched complement)
            Seq primer: M13 FORWARD
            POLYA=Yes.

FEATURES             Location/Qualifiers
     source           1..721
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-AA1-zw-f-06-0-UI"
                     /dev_stage="adult"
                     /lab_host="DHI08 (Life Technologies)"
                     /clone_lib="UI-R-AA1"
                     /notes="Vector: pT73D-Pac (Pharmacia) with a modified
                     polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-AA1
                     library is a normalized library constructed from 16.5 dpc
                     rat atrium. The tag is a string of 5 nucleotides present
                     between the Not I site and the oligo-dr track. The
                     library was constructed as described by Bonaudo, Lennon
                     and Soares, Genome Research 6: 791-806, 1996. Tissue
                     provided by Jim Lin, Department of Biology, University of
                     Iowa.
                     TAG_TISSUE=atrium at 16.5 dpc
                     TAG_LIB=UI-R-AA1
                     TAG_SEQ=GATTCC"

ORIGIN
Query Match      45.3%; Score 490.4; DB 7; Length 721;
Best Local Similarity 87.4%; Pred. No. 2e-132;
Matches 549; Conservative 0; Mismatches 76; Indels 3; Gaps 1;

Qy      450  TTGTGGTATTGTTCGGTGCATCTCGCATGGCGCATGGCGTACTGCGCTCTCTTTGCCGCA 509
            |||||

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Db      721  TGGTGGTATTGTTCGGTGCATGGCGTGTGGCTGCGCGACTCTCTTTGCCGCA 662
Qy      510  GTCTGTGTTTTTATGAGCCTCGGATGGAAGACAGAAACACAAGTGTGCCCTTTGGCAAAAC 569
            |||||
Db      661  AGCTGTGTTTTTACGAGCCTCGGATGGAAGACAGAAACACAAGTGTGGCTTTGGCAAAAC 602
Qy      570  TCATCTCTTTGCCAATCGAAGCGCGCTCTGGAAGTACGTTCTGACCTCAAAATGATCAT 629
            |||||
Db      601  TCATCTCTTTGCAATTAAGACACCGATCTGGAAGTATGTTCTGACTTCAAGATGAACAT 542
Qy      630  CTTGTGACTTGTCTCTCTGCTGCTTTTATAATATCTGCTGAGCAACATGAGGAGAAG 689
            |||||
Db      541  CTTGTGACTTGTCTCTCTGCTGCTTTTATATTCTGCTGAGGCAATGAGGACAGC 482
Qy      690  GCAGAGCTTTCAGGAGACAGATACACCTTCCAAAGCGCGCTTGTCTATACGCGCGT 749
            |||||
Db      481  GCAGAACTTTCAGGAGAGGAGCGACCTCCGAAGGCTGCTTGTCTATAACGGGTGT 422
Qy      750  GTTCTCTTTTGTATGTGGGCGCTTTACAACTGCTGCTTTTCTGCTGCTTTTCCAGGAACA 809
            |||||
Db      421  GTTCTCTTTTGTATGTGGGCGCTTACAACTGCTGCTTTTCTGCTGCTTTTCCAGGAACA 362
Qy      810  CTTGTCCCTTCAGGATGAGAAGAGCAGCTACCACTGGAGCGCAAGTGTTCAGGTCAACA 869
            |||||
Db      361  CTTGTCCCTTCAGGATGAGAAGAGCAGCTACCTACCTGGAGCGCAAGCAAGGCTCACACA 302
Qy      870  GCTGGTAGCGACCACTGCTGCTGCTCAACCGCTGCTCTATTTGCTTCTTCCGCGGA 929
            |||||
Db      301  GCTCATTTGGGACCACTGCTGCTGCTCAACCGCTGCTCTATTTGCTTCTTCCGCGCA 245
Qy      930  GGCCTTTATGAGATACCTTTCGAGCGCTGTTCCACGGTGCATATGATATCCCTTATCAAAG 989
            |||||
Db      244  GGCCTTTAGAGCTATCTCTGAGCGCTGTTCCACGGTGTATGATCTCCCATTTCAAAG 185
Qy      990  TAGTGGAGCTATCAGCAAGCGCTCCAAAGGAGGTATGAGGAGCGCCCACTGAACGTGA 1049
            |||||
Db      184  TGGTAGGAGCTCTCAGCAAGAGAGCGCAAGGAGGTACAGCAGCGCCCATTTGAACGTGA 125
Qy      1050  CAGCATTTTGCATCAAGGAGGAGGATATA 1077
            |||||
Db      124  CGGTACTTTTGGCTCAAAAGGAGGATATA 97
            |||||

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RESULT 10
AI876375      474 bp      mRNA      linear      EST 21-JUL-1999
LOCUS      uk74c03.y1 Schiller mouse At20 Mus musculus cDNA clone
DEFINITION  IMAGE:1974724 5', similar to TR:O35457 O35457 PUTATIVE BETA
            CHEMOKINE RECEPTOR. [1], mRNA sequence.
ACCESSION  AI876375
VERSION     AI876375.1 GI:5550424
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 474)
REFERENCE  1
AUTHORS    Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
            The WashU-NCI Mouse EST Project 1999
            Unpublished (1999)
            Contact: Marra M/WashU-NCI Mouse EST Project 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouesest@watson.wustl.edu
            This clone is available royalty-free through LML; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:991464

```

Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 397.

FEATURES

Location/Qualifiers
1..474

source

/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:1974724"
/cell_line="pituitary cell line"
/lab_host="SOLR"
/clone_lib="Schiller mouse At720"
/note="Organ: pituitary; Vector: pBluescript SK-
(stratagene); Site 1: EcoRI; Site 2: XhoI; Double-stranded
cDNA was prepared from cell line At7-20 using primer
5'-GAGAGAGAGAGAGAGAGAGAGTCTGAGT(18)-3'. An EcoRI
adaptor was used on the 5' end of the cDNA as follows:
5'-AATTCGGACGAG-3'. The library was size-selected and
went through one round of amplification. Average insert
size is 1.7 kb, with a range from 0.4-12 kb. This library
was constructed by Dr. Martin Schiller (Johns Hopkins
University)."

ORIGIN

Query Match 42.9%; Score 464.4; DB 1; Length 474;
Best Local Similarity 98.7%; Pred. No. 7.8e-125;
Matches 468; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 37 GATGCTCTTAATCTTAGACGACTACTGACACAGTGGCGCGGACCAAGTTCGGCCCCC 96
DB 1 GATGCTCTTAATCTTAGACGACTACTGACACAGTGGCGCGGACCAAGTTCGGCCCCC 60

QY 97 GAGTTCCTCTCCCCCAGCAGTGTCTGCTGCGGCTGTTCGGTGGGTCTC 156
DB 61 GAGTTCCTCTCCCCCAGCAGTGTCTGCTGCGGCTGTTCGGTGGGTCTC 120

QY 157 TTGGACAACTGCTGGCGGTGTTATCTTGGTGAATAACAAAGGACTCAAGAATCTGGGG 216
DB 121 TTGGACAACTGCTGGCGGTGTTATCTTGGTGAATAACAAAGGACTCAAGAATCTGGGG 180

QY 217 AACATCTACTTCTTAACTGCTGCTTCAACCTGTGTTCTGCTTCCCTGCGCTC 276
DB 181 AACATCTACTTCTTAACTGCTGCTTCAACCTGTGTTCTGCTTCCCTGCGCTC 240

QY 277 TGGGCCCCATCTGCAGCACACGGGAAAGCCCTGCGAAGGACTCTGTAAGTCTTCTC 336
DB 241 TGGGCCCCATCTGCAGCACACGGGAAAGCCCTGCTAATGGACCTGTAAGATCTTCTC 300

QY 337 GGACTCCACTCTCGGGCTTATACAGCGAGGTGTTTCCAAATCTCTCTCTTGTGCAA 396
DB 301 GGACTCCACTCTCGGGCTTATACAGCGAGGTGTTTCCAAATCTCTCTCTTGTGCAA 360

QY 397 GGATACAGGTGTTTCCCAAGGGGACCTGGCTTCAATCTTCAAGAGTGTCTTGGGT 456
DB 361 GGATACAGGTGTTTCCCAAGGGGACCTGGCTTCAATCTTCAAGAGTGTCTTGGGT 420

QY 457 ATTGTTGGTGCATCTCGCATGGCCATGCTACTGCGCTCTCTTTCGCCCGAG 510
DB 421 ATTGTTGGTGCATCTCGCATGGCCATGCTACTGCGCTCTCTTTCGCCCGAG 474

RESULT 11

BF662034 615 bp mRNA linear EST 20-DEC-2000
LOCUS msa77f10.y1 Soares mouse 3NBMS Mus musculus cDNA clone
DEFINITION IMAGE:3822882 5', similar to TR:035457 035457 PUTATIVE BETA
CHEMOKINE RECEPTOR. [1]; mRNA sequence.
ACCESSION BF662034
VERSION BF662034.1 GI:11927168
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS
TITLE

JOURNAL

COMMENT

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 615)
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Other ESTs: msa77f10.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:1459234

Seq primer: -40RP from Gibco

High quality sequence stop: 412.

FEATURES

source

Location/Qualifiers
1..615

/organism="Mus musculus"
/mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="IMAGE:3822882"
/sex="male"
/tissue_type="Spleen"
/dev_stages="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares mouse 3NBMS"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'.
TGTTACCAATCTGAAGTGGAGCGCGCTGTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through
three rounds of normalization, and was constructed by
Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 40.1%; Score 434; DB 2; Length 615;
Best Local Similarity 95.5%; Pred. No. 7.3e-116;
Matches 468; Conservative 0; Mismatches 20; Indels 2; Gaps 2;

QY 1 ATGGATAACTACACAGTGGCCCCCGACCGATGAATATGATGTCCTAATCTTAGACGACTAC 60
DB 127 ATGGATAACTACACAGTGGCCCCCGACCGATGAATATGATGTCCTAATCTTAGACGACTAC 186

QY 61 CTGACAAACAGTGGCGCGGACCAAGTTCGGCGCCCGGAGTTCCTCTCCCCCAGCAGGTG 120
DB 187 CTGACAAACAGTGGCGCGGACCAAGTTCGGCGCCCGGAGTTCCTCTCCCCCAGCAGGTG 246

QY 121 CTGCAGTTCCTCGCGGTGTTTGGCGGTGCTCTTGGCAACAGTGTCTGGCGGTGTTT 180
DB 247 CTGCAGTTCCTCGCGGTGTTTGGCGGTGCTCTTGGCAACAGTGTCTGGCGGTGTTT 306

QY 181 ATCTTGGTGAATAACAAAGGACTCAAGAATCTGGGGAAACATCTACTCTCTAAACCTGGCA 240
DB 307 ATCTTGGTGAATAACAAAGGACTCAAGAATCTGGGGAAACATCTACTCTCTAAACCTGGCA 366

QY 241 CTTTCAAACTGTGTTCTCTGCTTCCCTGCTTCCCGCTTCTGGGGCCATCTGCGAGCACACGG 300
DB 367 CTTTCAAACTGTGTTCTCTGCTTCCCTGCTTCCCGCTTCTGGGGCCATCTGCGAGCACACGG 426

QY 301 GAAAGCCCTGGCAACGGGACCTGTAAAGTTCCTTGGGACTCCACTCTCGGGCTTATAC 360
DB 427 GAAAGCCCTGGCAATGGACCTGTAAAGTTCCTTGAACGACTCCACTCTCGGGCTTATAC 486

QY 361 AGCGAGGTGTTTCCAAATCTCTCTCTTGTGTGCAAGGATACAGGGTGTGTTTCCAAAGG 420
DB 487 AGCGAGGTGTTTCCAAATCTCTCTCTTGTGTGCAATGATACAGGGTGTGTTT-CCATAGG 545

QY 421 CGACTGGCCTCCATCTTCAACGACAG-TGTCTTGTGTTATGTTGCGTGCATCTCGGCATG 479
DB 546 CGACTGGCCTACATCTTTAACGACACGCGTCTTGTGGGATTTGTTGCGTGCATCTAGTAGT 605

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Qy 480 GGCCATGGCT 489
Db 606 GGCCATGGT 615

RESULT 12
LOCUS CB598882
DEFINITION AGENCOURT_12785094 NIH_MGC_178 Mus musculus cDNA clone
IMAGE:30295418 5', mRNA sequence.
CB598882
ACCESSION CB598882.1 GI:29516738
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 721)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-x@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM53 row: b column: 03
High quality sequence stop: 541.
FEATURES
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            /clone_lib="NIH_MGC_178"
            /notes="Organ: lung and heart; Vector: pDNR-LIB; Site 1:
            SfiI (ggccatcgcc); Site 2: SfiI (ggccgctcgcc); cDNA
            made by oligo-dT priming and directionally cloned. 5' and
            3' adaptors were used in cloning as follows:
            5'-AAGCAGTGGTATCAACGAGTGGCCATTACGCCGGG-3', and
            5'-ATTCTAGAGCGGCGGCACATG-dT(30)NN-3'. Full-length
            enriched library was constructed using the Clontech
            Creator SMART kit and size-selected to contain the 0.5 kb
            size fraction. Library created in the laboratory of M.
            Brownstein (NIMH, NIH). Note: this is a NIH_MGC library."

ORIGIN
Query Match 39.3%; Score 425.6; DB 6; Length 721;
Best Local Similarity 93.2%; Pred. No. 2.2e-113;
Matches 466; Conservative 0; Mismatches 31; Indels 3; Gaps 2;

Qy 1 ATGATTAATCTACAGTGGCCCGGACGATGATATGATCTCTAATCTTAGACGACTAC 60
Db 172 ATGATAAATCTACAGTGGCCCGGACGATGATATGATCTCTAATCTTAGACGACTAC 231
Qy 61 CTGGACAACAGTGGCCCGGACCAAGTTCCGCGCCCGGAGTTCTCTCCCGCCGAGCGGTG 120
Db 232 CTGGACAACAGTGGCCCGGACCAAGTTCCGCGCCCGGAGTTCTCTCCCGCCGAGCGGTG 291
Qy 121 CTGCAGTCTCTGCTGCGCGGTGTTTGGCGGTGGGTCTCTTGACAACGTCGTGGCGGTGTTT 180
Db 292 CTGCAGTCTCTGCTGCGCGGTGTTTGGCGGTGGGTCTCTTGACAACGTCGTGGCGGTGTTT 351
Qy 181 ATCTTGTTGAATACAAAGACTCAAGAACTCTGGGGAACATCTACTTCTTAAACCTGGCA 240
Db 352 ATCTTGTTGAATACAAAGACTCAAGAACTCTGGGGAACATCTACTTCTTAAACCTGGCA 411

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Qy 241 CTTTCAAACTGTGTTTCTGCTTCCCTGCGCTTCTGGCCCACTACTGACACACGGG 300
Db 412 CTTTCAAACTGTGTTTCTGCTTCCCTGCGCTTCTGGCCCACTACTGACACACGGG 471
Qy 301 GAAAGCCCTGGCAACCGGACCTGTAAAGTCTTGTGGACTCCACTCCTCGGGC-TTATA 359
Db 472 GAAAGCCCTGGCAATCGGACCTGTAAAGTCTTGTGGACTCCACTCCTCGGGCNTTATA 531
Qy 360 CAGCAGAGTGTGTTTCCAAACATCTCTCTCTGTGCAAGGA--TACAGGAGTGTTCCTCCAA 417
Db 532 CAGCAGAGTGTGTTTCCAAACATCTCTCTCTGTGCAAGGAATACAGGGGTGTTTTCNCAA 591
Qy 418 GGGCGACTGGCCTCCCATCTTCACGACAGTGTCTTGTGGTATTGTTGGTGCATCTCGGCA 477
Db 592 GGGCGACTGGCCTCCCATCTTCACGACAGTGTCTTGTGGTATTGTTGGTGCATCTCG 651
Qy 478 TGGGCCATGGCTACTCGGCT 497
Db 652 TGGGCCATGGGCCATGGGCT 671

RESULT 13
LOCUS CA578957
DEFINITION K0730H02-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-)
IMAGE:30076501 5', mRNA sequence.
CA578957
ACCESSION CA578957.1 GI:25127348
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 554)
Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Carter,M.G.,
Aiba,K., Taub,D., Longo,D.L., Keller,J. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Hematopoietic Stem Cell
(Lin-/c-Kit-/Sca-1-) cDNA Library (Long)
Unpublished (2001)
Other ESTs: K0730H02-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
233 Caswell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igun.grc.nia.nih.gov
Plate: K0730 row: H column: 02
Seq primer: M13 Reverse
High quality sequence stop: 554
POLYA=No.
FEATURES
    Location/Qualifiers
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        /clone="NIA:K0730H02 IMAGE:30076501"
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        /lab_host="DH10B"
        /clone_lib="NIA Mouse Hematopoietic Stem Cell
        (Lin-/c-Kit-/Sca-1-) cDNA Library (Long)"
        /notes="Vector: pSPOT1 (Invitrogen); Site_1: SalI; Site_2:
        NotI; Mouse cDNA project by the Laboratory of Genetics,
        National Institute on Aging (NIA), Intramural Research
        Program, NIH (http://igun.grc.nia.nih.gov/cDNA). This is
        a long-transcript enriched cDNA library (Ref. Genome Res.
        11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
        obtained from Drs. Dennis Taub, Dan Longo (National
        Institute on Aging, USA), Jonathan Keller (National Cancer
        Institute, USA). Double-stranded cDNAs were synthesized

```

with an Oligo(dT) primer [Invitrogen:
5'-GGACTAGTCTAGATCGGAGCGCGCTTTT-3'] from
0.9 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to Lona-linker LL-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.1 kb. The library was constructed
by Yulan Piao (NIA)."

ORIGIN

Query Match	39.2%;	Score	424.4;	DB	6;	Length	554;		
Best Local Similarity	99.8%;	Pred. No.	4.7e-113;						
Matches	425;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	1	ATGGATAACTACACAGTGGCGCGGACGATGAATATGATGCTCTAAATCTTTAGACGACTAC	60						
Db	129	ATGGATAACTACACAGTGGCGCGGACGATGAATATGATGCTCTAAATCTTTAGACGACTAC	188						
Qy	61	CTGGACAAACAGTGGCGCGGACCAAGTTCGGCGCCCGAGTTCTCTCTCCCGCCGACGAGGTG	120						
Db	189	CTGGACAAACAGTGGCGCGGACCAAGTTCGGCGCCCGAGTTCTCTCTCCCGCCGACGAGGTG	248						
Qy	121	CTGCAGTTCGTCTGCGCGGTGTTTGGCGGTGGGTCTCTTTGGACAACGTCGTGGCGGTGTTT	180						
Db	249	CTGCAGTTCGTCTGCGCGGTGTTTGGCGGTGGGTCTCTTTGGACAACGTCGTGGCGGTGTTT	308						
Qy	181	ATCTTGGTGAATACAAAGGACTCAAGAACTCTGGGGAACATCTACTCTCTAAACCTGGCA	240						
Db	309	ATCTTGGTGAATACAAAGGACTCAAGAACTCTGGGGAACATCTACTCTCTAAACCTGGCA	368						
Qy	241	CTTTCAAACTGTGTTTCTGCTTCCCTGCGGTTCTGGGCGCCATCTGCGACACACGGG	300						
Db	369	CTTTCAAACTGTGTTTCTGCTTCCCTGCGGTTCTGGGCGCCATCTGCGACACACGGG	428						
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Db	429	GAAGCCCTGGCAATGGGACCTGTAAAGTTCTTGTGCGACTCCACTCTCGGGCTTATAC	488						
Qy	361	AGCGAGGTGTTTTCCAAACATCTCTCTTTGCGAAGGATACAGGGTGTTCCTCCCAAGGG	420						
Db	489	AGCGAGGTGTTTTCCAAACATCTCTCTTTGCGAAGGATACAGGGTGTTCCTCCCAAGGG	548						
Qy	421	CGACTG 426							
Db	549	CGACTG 554							

RESULT 14
CA580283
LOCUS
DEFINITION
K0749D08-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-)
CDNA Library (Long) Mus musculus CDNA clone NIA:K0749D08
IMAGE:30078283 5', mRNA sequence.
CA580283
CA580283.1 GI:25128674
EST.
Mus musculus (house mouse)
ORGANISM
Mus musculus
REFERENCE
1 (bases 1 to 552)
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G.,
Alba, K., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H.
Systematic Analyses of NIA Mouse Hematopoietic Stem Cell
(Lin-/c-Kit-/Sca-1-) cDNA Library (Long)
Unpublished (2001)

COMMENT

Other ESTs: K0749D08-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgun-grc.nia.nih.gov
Plate: K0749 row: D column: 08
Seq primer: M13 Reverse
High quality sequence stop: 552
POLYA-No.

FEATURES

source

Location/Qualifiers

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/db_xref="taxon:10090"
/clones="NIA:K0749D08 IMAGE:30078283"
/tissue_type="Hematopoietic Stem Cell"
/lin-/c-Kit-/Sca-1-)
/dev_stage="Age approx.10 weeks old"
/lab_hosts="DH10B"
/clone_lib="NIA Mouse Hematopoietic Stem Cell"
/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgun-grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
obtained from Drs. Dennis Taub, Dan Longo (National
Institute on Aging, USA), Jonathan Keller (National Cancer
Institute, USA). Double-stranded cDNAs were synthesized
with an Oligo(dT) primer (Invitrogen:
5'-GGACTAGTCTAGATCGGAGCGCGCTTTT-3') from
0.9 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to Lona-linker LL-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.1 kb. The library was constructed
by Yulan Piao (NIA)."

ORIGIN

Query Match	37.5%;	Score	406.6;	DB 6;	Length	552;			
Best Local Similarity	99.0%;	Pred. No.	8e-108;						
Matches	409;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;
Qy	1	ATGGATAACTACACAGTGGCGCGGACGATGAATATGATGTCCTAATCTTAGACGACTAC	60						
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Qy	61	CTGGACAAACAGTGGCGCGGACCAAGTTCGGCGCCCGGAGTTCCTCTCCCCCAGCAGGTG	120						
Db	200	CTGGACAAACAGTGGCGCGGACCAAGTTCGGCGCCCGGAGTTCCTCTCCCCCAGCAGGTG	259						
Qy	121	CTGCAGTTCGTGCGCGGCTGTTTGGCGTGGGTCTCTTGGACAAACGTGCTGGCGGTGTTT	180						
Db	260	CTGCAGTTCGTGCGCGGCTGTTTGGCGTGGGTCTCTTGGACAAACGTGCTGGCGGTGTTT	319						
Qy	181	ATCTTGGTGAATAACAAAGGACTCAAGAACTCTGGGGAACATCTACTCTCTAAACCTGGCA	240						
Db	320	ATCTTGGTGAATAACAAAGGACTCAAGAGTCTGGGGAACATCTACTCTCTAAACCTGGCA	379						
Qy	241	CTTTCAAAACCTGTGTTTCTGTTCCCTCGCGGTTCTGGGCCCATATCTGCAGACACACGGG	300						
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QY 301 GAAAGCCCTGGCAACGGACCTGTAAAGTTCTTGTGGAGCTCCACTCCTCGGCTTATAC 360
Db 440 GAAAGCCCTGGCAATGGGACCTGTAAAGTTCTTGTGGAGCTCCACTCCTCGGCTTATAC 499
QY 361 AGCGAGGTGTTTCCACATCTCCCTCTGTGTCAGGATACAGGGTGTTC 413
Db 500 AGCGAGGTGTTTTCACATCTCCCTCTGTGTCAGGATACAGGGTGTTC 552

RESULT 15
CA579095
LOCUS
DEFINITION
K0732G02-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-kit-/Sca-1-)
IMAGE:30076681 5', mRNA sequence.
CA579095
CA579095.1 GI:25127486
EST.
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 526)
Piao Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G.,
Aiba, K., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H.
Systematic Analyses of NIA Mouse Hematopoietic Stem Cell
(Lin-/c-kit-/Sca-1-) cDNA Library (Long)
Unpublished (2001)
Other ESTs: K0732G02-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgun.grc.nia.nih.gov
Plate: K0732 row: G column: 02
Seq primer: M13 Reverse
High quality sequence stop: 526
POLYA=No.

FEATURES
source

1. 526
/organism="Mus musculus"
/mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="NIA:K0732G02 IMAGE:30076681"
/tissue_type="Hematopoietic Stem Cell
(Lin-/c-kit-/Sca-1-)"
/dev_stage="Age approx.10 weeks old"
/lab_hosts="DHI08"
/clone_lib="NIA Mouse Hematopoietic Stem Cell
(Lin-/c-kit-/Sca-1-) cDNA Library (Long)"
/note="Vector: pSPORT1 (Invitrogen); Site 1: Sali; Site 2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
obtained from Drs. Dennis Taub, Dan Longo (National
Institute on Aging, USA), Jonathan Keller (National Cancer
Institute, USA). Double-stranded cDNAs were synthesized
with an Oligo(dT) primer [Invitrogen:
5'-pGACTATCTAGATCGAGCGCCCTTTT-3'] from
0.9 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to Lona-linker Li-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with Sali and NotI enzymes
and cloned into Sali/NotI site of pSPORT1 plasmid vector.

The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.1 kb. The library was constructed
by Yulan Piao (NIA)."

ORIGIN

Query Match 36.7%; Score 397.4; DB 6; Length 526;
Best Local Similarity 99.7%; Pred. No. 4e-105; Indels 0; Gaps 0;
Matches 398; Conservative 0; Mismatches 1;
QY 1 ATGGATAACTACACAGTGGCCCGGACGATGAATATGATCTCTTAATCTTTAGACGACTAC 60
Db 128 ATGGATAACTACACAGTGGCCCGGACGATGAATATGATCTCTTAATCTTTAGACGACTAC 187
QY 61 CTGGACAAACAGTGGGGCGGACCAAGTTCGGCCCCCGAGTTCTCTCCCCCAGCAGGTG 120
Db 188 CTGGACAAACAGTGGGGCGGACCAAGTTCGGCCCCCGAGTTCTCTCCCCCAGCAGGTG 247
QY 121 CTGCAGTCTTCTGTCGCGGGTGTGCGGTGGGTCTCTTGGACAAACGTGCGGGGTGTTT 180
Db 248 CTGCAGTCTTCTGTCGCGGGTGTGCGGTGGGTCTCTTGGACAAACGTGCGGGGTGTTT 307
QY 181 ATCTTGGTGAATATACAAAGGACTCAAGAATCTGGGGAACATCTTCTTAAACCTGGCA 240
Db 308 ATCTTGGTGAATATACAAAGGACTCAAGAATCTGGGGAACATCTTCTTAAACCTGGCA 367
QY 241 CTTTCAAACTGTGTTTCTGCTTCCCTGCGGTTCTGGGCCCCATCTGCGACACACGGG 300
Db 368 CTTTCAAACTGTGTTTCTGCTTCCCTGCGGTTCTGGGCCCCATCTGCGACACACGGG 427
QY 301 GAAAGCCCTGGCAACGGACCTGTAAAGTTCTTGTGGAGCTCCACTCCTCGGGCTTATAC 360
Db 428 GAAAGCCCTGGCAACGGACCTGTAAAGTTCTTGTGGAGCTCCACTCCTCGGGCTTATAC 487
QY 361 AGCGAGGTGTTTTCACACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 399
Db 488 AGCGAGGTGTTTTCACACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 526

Search completed: June 18, 2005, 12:08:00
Job time : 4144.74 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 18, 2005, 06:41:10 ; Search time 208.112 Seconds
(without alignments)
8515.071 Million cell update/sec

Title: US-10-623-472-32

Perfect score: 1083

Sequence: 1 atggataactacacagtggc.....aaaggcaggataataataa 1083

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA.*
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	421.6	38.9	1270	4	US-09-016-434-756 Sequence 756, App
2	420.4	38.8	1547	4	US-10-039-659A-11 Sequence 11, Appl
3	398.4	36.8	1050	3	US-08-681-192-1 Sequence 1, Appl
4	184.8	17.1	1059	4	US-08-771-276-19 Sequence 19, Appl
5	183.2	16.9	1065	3	US-08-847-296B-2 Sequence 2, Appl
6	183.2	16.9	1068	4	US-08-826-509-474 Sequence 474, App
7	183.2	16.9	1139	4	US-08-375-199B-3 Sequence 3, Appl
8	183.2	16.9	1193	4	US-08-720-565-3 Sequence 3, Appl
9	183.2	16.9	1201	4	US-08-016-434-1085 Sequence 1085, App
10	183.2	16.9	1201	4	US-09-023-655-905 Sequence 905, App
11	183.2	16.9	1717	4	US-09-023-655-959 Sequence 959, App
12	183.2	16.9	1915	3	US-08-575-967A-3 Sequence 3, Appl
13	183.2	16.9	1915	4	US-08-771-276-3 Sequence 3, Appl
14	180	16.6	1689	4	US-08-720-565-1 Sequence 1, Appl
15	180	16.6	1689	4	US-09-931-381A-15 Sequence 15, Appl
16	180	16.6	1689	4	US-08-375-199B-1 Sequence 1, Appl
17	179.6	16.6	1116	4	US-08-720-565-5 Sequence 5, Appl
18	179.6	16.6	1116	4	US-08-375-199B-5 Sequence 5, Appl
19	179.2	16.5	1071	4	US-08-567-882-6 Sequence 6, Appl
20	178.6	16.5	1059	3	US-08-724-984A-3 Sequence 3, Appl
21	178.6	16.5	1225	4	US-09-023-655-967 Sequence 967, App
22	178.6	16.5	1376	3	US-09-087-232A-12 Sequence 12, Appl
23	178.6	16.5	1376	4	US-09-016-434-1104 Sequence 1104, App
24	178.6	16.5	1376	4	US-08-795-202-2 Sequence 2, Appl
25	178.6	16.5	1414	4	US-09-502-783A-1 Sequence 1, Appl
26	178.6	16.5	1414	4	US-09-502-784A-1 Sequence 1, Appl
27	178.6	16.5	1414	4	US-09-339-912A-1 Sequence 1, Appl

28	178.6	16.5	1414	4	US-09-195-662A-1 Sequence 1, Appl
29	178.6	16.5	1477	3	US-08-833-752-2 Sequence 2, Appl
30	178.6	16.5	1477	4	US-09-938-719-2 Sequence 2, Appl
31	178.6	16.5	1477	4	US-09-939-226B-2 Sequence 2, Appl
32	178.6	16.5	3383	3	US-08-861-105-13 Sequence 13, Appl
33	178.6	16.5	3383	3	US-08-575-967A-1 Sequence 1, Appl
34	178.6	16.5	3383	4	US-09-023-655-951 Sequence 951, App
35	178.6	16.5	3383	4	US-08-771-276-1 Sequence 1, Appl
36	178.6	16.5	5674	4	US-09-293-170-3 Sequence 3, Appl
37	177	16.3	1059	4	US-08-826-509-476 Sequence 476, App
38	177	16.3	1071	3	US-09-087-232A-14 Sequence 14, Appl
39	175.2	16.2	1414	3	US-08-486-343D-1 Sequence 1, Appl
40	173.8	16.0	1059	3	US-09-517-605-8 Sequence 8, Appl
41	167.4	15.5	1495	4	US-09-016-434-1190 Sequence 1190, App
42	167.4	15.5	1495	4	US-09-023-655-1021 Sequence 1021, App
43	167.4	15.5	2156	1	US-08-012-988A-1 Sequence 1, Appl
44	167.4	15.5	2156	4	US-09-023-655-1247 Sequence 1247, App
45	158	14.6	2772	4	US-09-919-039-171 Sequence 171, App

ALIGNMENTS

RESULT 1
US-09-016-434-756
; Sequence 756, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 845-4166
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 756:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1270 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: MPHGN0703
; CLONE: 442279
; US-09-016-434-756

Query Match 38.9%; Score 421.6; DB 4; Length 1270;
Best Local Similarity 65.4%; Pred. No. 1.5e-124;

Db 484 CACAAGGCGACATTTTCTCAGCAGGAGGAGGTCCTCTGGCATCATTTACAAGTGC 543
Qy 472 CTGCGATGGGCGCATGGCTACTCGCGTCTCTTTGGCCGAGTCTGTGTTTATGAGCCTCGG 531
Db 544 CTGCGATGGGTAACAGACCATTTCTGCCACTTTGCGCTGAATTCGTGGTTTATAAACCTCAG 603
Qy 532 ATGGAAGACAGAAACACAACTGTGCTTTTGGCAAACTCACTTCTTGCCCAATCGAAGCG 591
Db 604 ATGGAAGACAGAAATACAACTGTGCTTTTACGAGAACTCCTTCTGCCAGCTGTATGAG 663
Qy 592 CCGCTCTGGAAGTACGTTCTGACGTCAAAATGATCATCTTGTGTAATCTTTTCCCTG 651
Db 664 ACATTCTGGAAGCATTTTCTGACTTTAAAAATGAACATTTCCGTTCTTGTCTCCCTC 723
Qy 652 CTGCTTTTATAATCTGCTGACGCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 711
Db 724 TTTATTTTATCATTTCTATGTGCAATGAGAAACACTAAGGTTTCAGGAGGAGGAGG 783
Qy 712 TACGACCTCCACAAAGCGGCTTGTCTATACGCGGCGTGTCTTCTTTGATGTGGCGCT 771
Db 784 TATAGCCTTTTCAAGCTTGTTTTGGCGTAATGTAGTCTTCTTCTGATGTGGCGGCC 843
Qy 772 TACAACACTGTGCTTTTCTGCTGCTTTCAGGAACACTTGTCTCCTGCAAGATGAGAAG 831
Db 844 TACAATATGCAATTTCTGCTGCTTTCAGGAACACTTTCCTCCTGAGTGAAGTGAAG 903
Qy 832 AGCAGCTACCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 891
Db 904 AGCAGCTACCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 963
Qy 892 TGCCTCAACCGCTGCTCTATTCTGCTTTCAGCGGAGGCTTTTATGAGATACCTTCGC 951
Db 964 TGCAATCAACCTCTCTGCTGATGCTTCTGATGCGA---CATTTAGCAATACCTCTGC 1020
Qy 952 AGCCTGTTCACCGGTGCAATGATATCCCTTATCAAAAGTGTGAGGAGGATCAACAAAGC 1011
Db 1021 CGCTGTTTCCATCTGCTGATGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCAAGGC 1080
Qy 1012 CTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1071
Db 1081 ACATCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
Qy 1072 GA 1073
Db 1141 GA 1142

RESULT 3

US-08-681-192-1
; Sequence 1, Application US/08681192
; Patent No. 6287801
; GENERAL INFORMATION:
; APPLICANT: BERGMA, DERK
; APPLICANT: ELSHOURBAGY, NABIL
; APPLICANT: SARAU, HENRY
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR HNFDS78
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/681,192

; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: ATG90014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5031
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1050 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; US-08-681-192-1

Query Match 36.8%; Score 398.4; DB 3; Length 1050;
Best Local Similarity 66.5%; Pred. No. 3.7e-117; Indels 33; Gaps 5;
Matches 662; Conservative 0; Mismatches 301;
Qy 1 ATGGAATACTACAGGTGGCCCGGACGATGAATATGATGTCTTAATCTTAGACGACTAC 60
Db 76 ATGSCCAATTACAGCTGGCCACGAGGATGAATATGATGTCC---TCATAGAAGGTGAA 132
Qy 61 CTGGAACAAGTGGCCGCGACCAAGTT-----CCGGCCCCCGAGTTCCTCTCCCCCAG 114
Db 133 CTGAGAGCGATGAGGAGAGCAATGTGACAAGTATGACGCCGAGGACTCTCAGCCAG 192
Qy 115 CAGGTCTGCGAGTCTGCTGCGGGTGTTCGGTGGTCTCTTGGGACAACTGCTGGCG 174
Db 193 CTGCTGCGATCCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 252
Qy 175 GTGTTATCTTGTGTAATAACAAGGACTCAAGAATCTGGGGAACATCTACTTCTTAAC 234
Db 253 GTGTTATCTTGTGTAATAACAAGGACTCAAGAATCTGGGGAACATCTACTTCTTAAC 312
Qy 235 CTGSCACTTTCAAACTGTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 294
Db 313 TTGGCAGTTTCTAACTTGTGTTTCTTGTCTTACCCTGCTCTCTGCGGCTCATGCTG 367
Qy 295 CACGGGGAAGCCCTGGCAACGGGACCTGTAAAGTCTTGTGCGACTCCACTCTCGGGC 354
Db 368 -----GGGCGGATCCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGTGGC 414
Qy 355 TTATACAGCAGGTGTTTTCACAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 412
Db 415 CTGTACAGTGAACATTTTCAATTTGCTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 474
Qy 413 -CCCAAGGCGACTGGCCTCCATCTTCAACAGAGTGTCTGTGTGTGTGTGTGTGTGTGT 471
Db 475 CACAAGGGCAACTTTTCTCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 534
Qy 472 CTGSCATGGGCCCATGGCTACTGCGCTCTCTTTCGCCGAGTCTGTGTTTATAGACCTCGG 531
Db 535 CTGCGATGGGTAAACAGCCATTTCTGGCCACTTTGCTGTAATTCGTGGTTTATAACCTCAG 594
Qy 532 ATGGAAGACAGAAACACAAAGTGTGCTTTTGGCAAACTCACTTCTTGTGCCAATCGAAGCG 591
Db 595 ATGGAAGACAGAAATACAAAGTGTGCTTTTATAGCAGAACTCCCTTCTGCCAGCTGATGAG 654
Qy 592 CCGCTCTGGAAGTACGTTCTGAGCTCAAAATGATCATCTTGTGTACTTGTCTTCTCTG 651
Db 655 ACATTCTGGAAGCATTTTCTGACTTTAAAAATGAACATTTCCGTTCTTGTCTCTCCCTCA 714


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; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Pabseq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,296B
; FILING DATE: 24-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/016,158
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 60/017,113
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Thies, J. Eric
; REGISTRATION NUMBER: 35,382
; REFERENCE/DOCKET NUMBER: 19634Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3904
; TELEFAX: 908-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1065 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-847-296B-2

Query Match      16.9%; Score 183.2; DB 3; Length 1065;
Best Local Similarity 54.3%; Pred. No. 4.9e-48;
Matches 446; Conservative 0; Mismatches 358; Indels 18; Gaps 3;

Qy 110 CCCAGCAGGCTGCAGTCTCTGCGGGGTTTGGCGGTGGTCTCTTGGACACGTC 169
Db 101 CCCAGTTTGTGCCCGCTGTACTCCCTGGTGTCTCTGCGGGCTCTTGGCAATGTG 160
Qy 170 TGGCGGTGTTTATCTTGGTGAATACAAAGACCTCAAGAACTCTGGGAACATCTACTTCC 229
Db 161 TGGTGGTGATGATCTCTATTAATACAGAGGCTCCGAAATATGACCAACATCTACTGC 220
Qy 230 TAAACCTGGCACTTTCAAACTGTGTTTCTGCTTCCCTGCGGTCTTGGGCCCACTG 289
Db 221 TCAACCTGGCACTTTGGAGGCTGTCTCTTCCCTGCTGACCTTCCATCTTGGATCCACTATG 280
Qy 290 ---CAGCACGGGAAGCCCTGGCACGGGACCTGTAAAGTCTTGTGCGACTCCACT 346
Db 281 TCAGGGGGCAATACTGGGTTTGGCCATGGCATGTGTAAAGTCTCTTCAGGGTTTATC 340
Qy 347 CCTGGGCTTATACAGCGAGGTGTTTCCAAACATCTCTCTTGTGTCAAGGATACAGGG 406
Db 341 ACACAGGCTGTACAGCGAGATCTTTTTCATATCTCTGCTGACCAATCGACAGGTACCTGG 400
Qy 407 TGTGTTCCCAAGGGGCACTGGCCCTCCATCTTTCACGACAGTGTCTTGTGCTTGTGCGT 466
Db 401 CCATTGTCATGCTGTGTTGCGCTTTCAGGCCGAGCTGTCACTTTTGGTGTCACTCA 460
Qy 467 GCATCTGGCATGGCCATGGCTACTGGCTCTCTTGGCCGAGTCTGTGTTTATGAGC 526
Db 461 GCATCTGACCTGGGGCTGGGAGTGTGAGCTCTTCTGCAATTTATCTTATGAGA 520
Qy 527 CTCGGATGGAAGACAGAAACACAAAGTGTGCTTTGGCAAACTCCACTCTTGTGCAATCG 586
Db 521 CT-----GAAGAGTTGTTGAGAGACTCTTTGAGTGTCTTTTACCCAGGAGATA 571
Qy 587 AAGCGCCGCTCTGGAAGTACGTTCTGACGTCAAAATGATCATCTTGTGTAATTGCTTTTC 646

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RESULT 6

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US-09-826-509-474
; Sequence 474, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: Patent in Version 2.1
; SEQ ID NO 474
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-474

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Query Match      16.9%; Score 183.2; DB 4; Length 1068;
Best Local Similarity 54.3%; Pred. No. 4.9e-48;
Matches 446; Conservative 0; Mismatches 358; Indels 18; Gaps 3;

Qy 110 CCCAGCAGGCTGCAGTCTCTGCGGGTGTGCGGGTGGTCTCTTGGACACGTC 169
Db 101 CCCAGTTTGTGCCCGCTGTACTCCCTGGTGTCTCTGCGGGCTCTTGGCAATGTG 160
Qy 170 TGGCGGTGTTTATCTTGGTGAATACAAAGACCTCAAGAACTCTGGGAACATCTACTTCC 229
Db 161 TGGTGGTGATGATCTCTATTAATACAGAGGCTCCGAAATATGACCAACATCTACTGC 220
Qy 230 TAAACCTGGCACTTTCAAACTGTGTTTCTGCTTCCCTGCGGTCTTGGGCCCACTG 289
Db 221 TCAACCTGGCACTTTGGAGGCTGTCTCTTCCCTGCTGACCTTCCATCTTGGATCCACTATG 280
Qy 290 ---CAGCACGGGAAGCCCTGGCACGGGACCTGTAAAGTCTTGTGCGACTCCACT 346
Db 281 TCAGGGGGCAATACTGGGTTTGGCCATGGCATGTGTAAAGTCTCTTCAGGGTTTATC 340
Qy 347 CCTGGGCTTATACAGCGAGGTGTTTCCAAACATCTCTCTTGTGTCAAGGATACAGGG 406
Db 341 ACACAGGCTGTACAGCGAGATCTTTTTCATATCTCTGCTGACCAATCGACAGGTACCTGG 400
Qy 407 TGTGTTCCCAAGGGGCACTGGCCCTCCATCTTTCACGACAGTGTCTTGTGCTTGTGCGT 466

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720.565
FILING DATE: 30-SEP-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00608
FILING DATE: 19-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375.199
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS94-05A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1193 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 92..1156
US-08-720-565-3

Query Match 16.9%; Score 183.2; DB 4; Length 1193;
Best Local Similarity 54.3%; Pred. No. 5.2e-48;
Matches 446; Conservative 0; Mismatches 358; Indels 18; Gaps 3;

110 CCCAGCAGGCTGCTCAGTCTGCTGCGCGGTGTTGGCGGTCTCTTGACAACTGC 169
192 CCCAGTTGTGCCCCCGCTGTACTCCCTGTGTTTCACTGTGGGCTCTTGGGCAATG 251
170 TGGCGGTGTTTATCTTGGTGAATATACAAAGACTCAAGAAATCTGGGAAATCTACTTCC 229
252 TGGTGGTGATGATCCTCATAAATACAGGAGCTCCGAATATATACCAACATCTACCTGC 311
230 TAACTGGCACTTTCAAACTGTGTTCTGCTTCCCTGCCCTTCTGGGCCATCTG 289
312 TCAACCTGGCCATTTCCGACCTGCTCTTCTCTGTCGTCACCTTCCATTTGGATCCACTATG 371
290 ---CAGCACACGGGGAAGCCCTGGCAAGGAGCTGTAAAGTTCTTGTGCGACTCCACT 346
372 TCAGGGGGCATACTGGGTTTTTGGCCATGCGATGTGTAGCTCTCTCAGGGTTTATC 431
347 CCTCGGCTTATACAGCGAGTGTGTTTCCAAATCTCTCTCTTGTGCAAGGATACAGG 406
432 ACACAGGCTTGTACAGCGAGATCTTTTTCATATCTCTGCTGACAATACAGAGGTACCTGG 491
407 TGTTTTCCCAAGGGGAGTGGCTTCCATCTTCACGACAGTGTCTTGTGGTATGTTGGGT 466
492 CCATTGTCCATGCTGTGTTGTCCTTCGAGCCGGAGTGTCACTTTTGGTGTCAACCA 551
467 GCATCTGGGATGGGCGCATGCTACTGCGCTCTCTTTGCGGAGTCTGTGTTTTATGAGC 526
552 GCATCTGTCACCTGGGCTGGCAGTGTAGCAGTCTCTCTGAAATTTATCTTCTATGAGA 611
527 CTCGGATGGAAGACAGAAACACAAGTGTGCTTTGGCAACCTCACTTCTTGGCAATCG 586
612 CT-----GAAGAGTGTGTTGAAGAGACTCTTTGCAAGTGTCTTTTACCCAGAGATA 662
587 AAGCGCGCTCTGGAAGTACGTTCTGAGTCAAAATGATCATCTTGGTACTGCTTTTC 646
663 CAGTATATAGCTGGAGGCAATTTCCACACTCTGTGAGAAATGACCATCTTCTGCTCGTCTCTCC 722

647 CTCTGCTGGTTTTTATATCTGCTGAGGCAACTGAGGAGAGGC-----AGAGCTTCA 700
723 CTCTGCTGTTATGGCCATCTGCTACACAGAAATCATCAAAACGCTGCTGAGGTGCCCCA 782
701 GGGAGAGACAGTACGACCTCCACAAGCGGCTCTTGTCTATAACGGGCGTGTCTCTTTGA 760
783 GTAAAAAAGTACAGGCCCATCGGCTCATTTTTTGTCTATCATGCGGCTGTTTTTCATT 842
761 TGTGGCGGCTTACAACTGCTGCTTTCTGCTGCTTTCTGCTGCTTTCCAGGAACACTTGTCCCTGC 820
843 TCTGGACACCTACATGTTGGCTATCTTCTCTCTCTATCATCATCATCTTATTTGAA 902
821 AGGATGAGAGAGAGAGTACCACTGACGACCAAGTGTTCAGGTCAACAGCTGTGTAGCA 880
903 ATGACTGTGAGCGGAGCAAGCATCTGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 962
881 CCACCACTGCTGCTCAACCGGCTGCTCTATTTGCTTCTTG 922
963 ACTCCCACTGCTGATCAACCGGCTGATCTACGCTTTGTTG 1004

RESULT 9
US-09-016-434-1085
; Sequence 1085, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016.434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1085:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1201 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1199579
; US-09-016-434-1085

Query Match 16.9%; Score 183.2; DB 4; Length 1201;
Best Local Similarity 54.3%; Pred. No. 5.3e-48;
Matches 446; Conservative 0; Mismatches 358; Indels 18; Gaps 3;

110 CCAGCAGAGTGTGACAGTCTCTGCTGGCGGTGTTGGGTGCTCTTTGGACAACGTGC 169
132 CCAGTTTGTGCCCCCTGTACTCTCCCTGTGTCTACTGTGGGCTCTTGGCAATGTGG 191
170 TGGCGGTGTTTATCTTGGTGAATACAAAGAGCTCAAGAAATCTGGGGAACATCTACTTCC 229
192 TGGTGGTGAATCTCATTAATACAGAGGCTCCGAATATGACCAACATCTACTTGC 251
230 TAAACCTGGCACTTTCAAACTGTGTCTGCTTCCCTTGGCGGTCTGGGCCCACTG 289
252 TCAACCTGGCACTTTGGAGCTGTCTCTCTGCTGACCCCTTCCATCTGGATCCACTG 311
290 ---CAGCACACGGGAAAGCCCTGGCAACGGGAGCTGTAAGTCTTGTGCGACTCCACT 346
312 TCAGGGGGCACTAGTGGTTTTGGCCATGGCATGTGTAGTCTCTCAGGGTTTATC 371
347 CTTGGGCTTATACAGCGAGGTGTTTTCAACATCTCTCTCTTGTGCAAGGATACAGGG 406
372 ACAGAGCTTGTACAGCGAGATCTTTTTCATAATCTCTGCTGACAAATGACAGAGTACCTGG 431
407 TGTTTTCCCAAGGGGAGTGGCTCCATCTTACGACAGTGTCTTGGGTATTTGTCGT 466
432 CCATTTGCTATGCTGTGTTTTGCCCTTCGAGCCGAGCTGTCACTTTTGGTGTCAACCA 491
467 GCATCTCGCATGGCCATGGCTACTGCTCTCTTTGCCGAGTCTGTGTTTTATGAGC 526
492 GCATCTGCTACCTGGGCTGGAGTGTAGAGTCTTCTGAAATTAATCTTCTATGAGA 551
527 CTCGGATGGAAGACAGAAACACAAAGTGTGCTTTGGCAACCTCACTTCTGCCAATCG 586
552 CT-----GAAGAGTGTGTTGAAGAGACTCTTTGCACTGTCTTTTACCCAGAGGATA 602
587 AAGCGCGCTCTGGAAGTACGTTCTGACGTCAAAATGATCATCTTGGTACTTCTTTC 646
603 CAGTATATAGCTGGAGCATTTCCACACTCTGGAATGACCATCTTCTGTCTGTTCTCC 662
647 CTCTGCTGTTTTTATTAATCTGCTGACAGCAACTGAGGAAAGC-----AGAGCTTCA 700
663 CTCTGCTGTTATGGCCATCTGTACACAGAAATCATCAAAAGCTGTGAGTGGCCCA 722
701 GGGAGAGACAGTACGACCTCCACAGCGGCTCTTGTATACAGCGGCTTTCTTTTGA 760
723 GTAAAAAAGTACAGGCCATCGGCTCATTTTGTGATCATGCGGCTGTTTTTCATTT 782
761 TGTGGGCGCTTACACACTGTGCTTTCTGCTGCTTTTCCAGGAACACTTCTCCCTGC 820
783 TCTGGACACCTACAAATGTGGCTATCTCTCTCTCTATCAATCCATCTTATTTGGAA 842
821 AGGATGAGAAGAGCAGCTACACCTGGACGCAAGTGTTCAGGTACACAGCTGCTAGCGA 880
843 ATGACTGTAGCGGAGCAAGCATCTGGACCTGTGTCATGCTGTTGACAGAGTATGCTCT 902
881 CCACCCACTGCTGGTCAACCCGCTGCTCTATTGTTCTTG 922
903 ACTCCCACTGCTGATGAACCCGCTGATCTACGCCCTTTGTTG 944

RESULT 10

US-09-023-655-905
; Sequence 905, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; TITLE OF INVENTION: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA

COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 905:
SEQUENCE CHARACTERISTICS:
LENGTH: 1201 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1199579
US-09-023-655-905

Query Match 16.9%; Score 183.2; DB 4; Length 1201;
Best Local Similarity 54.3%; Pred. No. 5.3e-48;
Matches 446; Conservative 0; Mismatches 358; Indels 18; Gaps 3;

110 CCAGCAGAGTGTGACAGTCTCTGCTGGCGGTGTTGGGTGCTCTTTGGACAACGTGC 169
132 CCAGTTTGTGCCCCCTGTACTCTCCCTGTGTCTACTGTGGGCTCTTGGCAATGTGG 191
170 TGGCGGTGTTTATCTTGGTGAATACAAAGAGCTCAAGAAATCTGGGGAACATCTACTTCC 229
192 TGGTGGTGAATCTCATTAATACAGAGGCTCCGAATATGACCAACATCTACTTGC 251
230 TAAACCTGGCACTTTCAAACTGTGTGCTGCTTCCCTTGGCGGTCTGGGCCCACTG 289
252 TCAACCTGGCACTTTGGAGCTGTCTCTCTGCTGACCCCTTCCATCTTGGATCCACTG 311
290 ---CAGCACACGGGAAAGCCCTGGCAACGGGAGCTGTAAGTCTTGTGCGACTCCACT 346
312 TCAGGGGGCATTAATCTGGGTTTTTGGCCATGGCATGTGTAGTCTCTCAGGGTTTATC 371
347 CTTGGGCTTATACAGCGAGGTGTTTTCAACATCTCTCTCTTGTGCAAGGATACAGGG 406
372 ACAGAGCTTGTACAGCGAGATCTTTTTCATAATCTCTGCTGACAAATGACAGAGTACCTGG 431
407 TGTTTTCCCAAGGGGCACTGGCTCCATCTTACGACAGTGTCTTGGGTATTTGTCGT 466
432 CCATTTGCTATGCTGTGTTTTGCCCTTCGAGCCGAGCTGTCACTTTGTTGTCATCACA 491
467 GCATCTCGCATGGGCTGGCTACTGCTCTCTTTGGCCGAGTCTGTGTTTTATGAGC 526
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527 CTCGGATGGAAGACAGAAACACAAAGTGTGCTTTGGCAACCTCACTTCTTCCCAATCG 586
552 CT-----GAAGAGTGTGTTGAAGAGACTCTTTGCACTGTCTTTTACCCAGAGGATA 602
587 AAGCGCGCTCTGGAAGTACGTTCTGACGTCAAAATGATCATCTTGGTACTTCTTTC 646
603 CAGTATATAGCTGGAGGCAATTTCCACACTCTGGAATGACCATCTTCTGTCTGTTCTCC 662

Db 462 CCCAGTTTGTGCCCCCGCTGTAACCTCCCTGGTGTCACTGTGGGCTCTTTGGCAATGTGG 521
Qy 170 TGGCGGTCTTATCTTGTGTAATCAAAAGAGCTCAAGAACTGGGGAACTACTTCTCC 229
Db 522 TGGTGGTGATGATCTCTATAAATAACAGAGGCTCGAATATGACCAACATCTACCTGC 581
Qy 230 TAAACCTGGCACTTTCAAACTGTGTTTCCCTGCTTCCCTGCGCTTCTGGGCCCACTATG 289
Db 582 TCAACCTGGCCATTTGGGACCTGCTCTTCCCTGCTGACCTTCCATCTCTGGATCCACTATG 641
Qy 290 ---CAGCACAGGGGAAGCCCTGCAAGGAGCTGTAAAGTCTTGTGCGACTCCACT 346
Db 642 TCAGGGGCAATAACTGGGTTTTTGGCCATGGCATGTGAAGCTCTCTCAGGGTTTTATC 701
Qy 347 CTCTGGGCTTATACAGCGAGGTGTTTTCCAACTCTCTCTCTGTGCAAGGATACAGG 406
Db 702 ACACAGGCTTGTACAGCGAGATCTTTTTCAATATCTCTGTACATCCAGAGGTACCTGG 761
Qy 407 TGTCTTCCAAAGGCGACTGCGCTCCATCTTTACGACAGTGTCTTGTGATTTGTTCGT 466
Db 762 CCATTGTCATGCTGTGTTGCTTCCCTTCGAGCCGAGCTGTCACTTTTGTGTCTATCACA 821
Qy 467 GCATCTGGCATGGCCATGGCTACTGCGCTCTCTTCCCGAGTCTGTGTGTTTTATGAGC 526
Db 822 GCATCGTCACCTGGGCGCTGCGAGTGTGAGAGCTCTTCTCAATTTATCTTCTATGAGA 881
Qy 527 CTCGGATGAAGAGCAGAAACACAGTGTGCTTTGGCAACCTCACTTCTTGCCAACTG 586
Db 882 CT-----GAAGAGTTGTTGAGAGATCTTTTGGAGTCTCTTGGAGTCTCTTACCCAGAGGATA 932
Qy 587 AAGCGCGCTCTGGAAGTACGTTCTGAGCTCAAAATGATCATCTTGTACTTGTCTTTTC 646
Db 933 CAGTATATAGCTGGAGGCAATTTCCACACTCTGAGAAATGACCACTCTTCTGTCTGTTCTCC 992
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Qy 761 TGTGGGCGCTTACAACTGTGCTGTTTTTCTGTCTGCTTCCAGGAAACATTTGCTCCCTGC 820
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RESULT 14

US-08-720-565-1
; Sequence 1, Application US/08720565
; Patent No. 6537764
; GENERAL INFORMATION:
; APPLICANT: Gerard, Craig J.
; APPLICANT: Gerard, No. 6537764ma P.
; APPLICANT: Mackay, Charles R.
; APPLICANT: Ponath, Paul D.
; APPLICANT: Post, Theodore W.
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
; TITLE OF INVENTION: ANTAGONISTS THEREOF
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive

; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,565
; FILING DATE: 30-SEP-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00608
; FILING DATE: 19-JAN-1996
; APPLICATION NUMBER: US 08/375,199
; FILING DATE: 19-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS94-05A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-720-565-1

Query Match 16.6%; Score 180; DB 4; Length 1689;
Best Local Similarity 54.0%; Pred. No. 7e-47;
Matches 444; Conservative 0; Mismatches 360; Indels 18; Gaps 3;

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Db 1052 ACTCCCACTGCTGATGAACCCGGTGAATCTACGGCTTTGTTG 1093

RESULT 15
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; Sequence 15: Application US/09931381A
; Patent No. 6692922
; GENERAL INFORMATION:
; APPLICANT: Butcher, Eugene C.
; APPLICANT: Kunkel, Eric J.
; APPLICANT: Pan, Junliang
; APPLICANT: Soler-Ferran, Dulce
; TITLE OF INVENTION: Method for Identifying Agents Which
; TITLE OF INVENTION: Modulate Chemokine "Mec"-Induced Functions of CCR3 and/or
; FILE OF INVENTION: CCR10
; FILE REFERENCE: 1855.2010-003
; CURRENT APPLICATION NUMBER: US/09/931.381A
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: U.S. 09/638,914
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1689
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (181)...(1248)
; NAME/KEY: misc feature
; LOCATION: (1291)...(1291)
; OTHER INFORMATION: n = A, T, C or G
US-09-931-381A-15
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Query Match 16.6%; Score 180; DB 4; Length 1689;
Best Local Similarity 54.0%; Pred. No. 7e-47;
Matches 444; Conservative 0; Mismatches 360; Indels 18; Gaps 3;

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Db 1052 ACTCCCACTGCTGATGAACCCCGGTGATCTACGGCTTTGTTG 1093
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 18, 2005, 09:53:05 ; Search time 755.748 Seconds
(without alignments)
8895.522 Million cell updates/sec

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Perfect score: 1083
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 6054689 seqs, 3103772919 residues

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	423.2	39.1	1776	21	US-10-741-600-13
4	423.2	39.1	14341	21	US-10-741-600-17557
5	422	39.0	1140	16	US-10-029-386-22780
6	422	39.0	1475	15	US-10-223-085-15
7	422	39.0	1475	15	US-10-223-084-15

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; Sequence 32, Application US/10623472
; Publication No. US20040096913A1
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Groningen
; APPLICANT: Boddeke, Erik H.W.G.M.
; APPLICANT: Biber, Knut
; TITLE OF INVENTION: Cloning and expression of a new MCP receptor in glial cells
; FILE REFERENCE: 2183-6042US
; CURRENT APPLICATION NUMBER: US/10/623.472
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: PCT/NL02/00039
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: EP 01200181.4
; PRIOR FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 1083
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1083)
; OTHER INFORMATION: mCCR12 chemokine receptor sequence
US-10-623-472-32
Query Match 100.0%; Score 1083; DB 18; Length 1083;
Best Local Similarity 100.0%; Pred. No. 0;

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QY 421 CGACTGSCCTCCATCTTTCAGACAGTGTCTGTGGTATGTTGCTGTCATCTCTGGCATGG 480
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DB 481 GCCATGCTACTGCGCTCTCTTTGCCGAGTCTGTGTTTATGAGCCTCGGATGGAAGA 540
QY 541 CAGAAACAAAGTGTGCTTTGGCAACCTCACTTCTTGCCAAATCGAAGCGCGCTCTGG 600
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QY 601 AAGTACGTTCTGAGTCAAAAATGATCATCTTGATGTTGCTTTCTCTGCTGGTGTGTTT 660
DB 601 AAGTACGTTCTGAGTCAAAAATGATCATCTTGATGTTGCTTTCTCTGCTGGTGTGTTT 660
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DB 661 ATAATCTGCTGCAGGCAACTGAGGAGAAAGCAGAGCTTCAGGGAGAGACATGACGCTC 720
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DB 1081 TAA 1083
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US-10-741-600-12
; Sequence 12, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1646
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-12
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Query Match 39.1%; Score 423.2; DB 21; Length 1646;

Best Local Similarity 65.2%; Pred. No. 1.5e-131; Indels 33; Gaps 5;

Matches 706; Conservative 5; Mismatches 338; Indels 33; Gaps 5;

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DB 259 CTGAGAGCGATGAGGACAGCAATGTGACAAGTATGACGCCAGGCACTCTCAGCCCCAG 318
QY 115 CAGGTCTGCAGTTCGTGCGCGGTGTTTGGGTGGTCTCTTGACAAACGTGCTGGCG 174
DB 319 CTGGTCCCATCACTGTCTGTCTGTGTTTGTATCGGTGCTCTGACAAATCTCTGTT 378
QY 175 GTGTTTATCTTGTGAAATACAAAGGACTCAAGAAATCTGGGAAACATCTACTTCTTAAAC 234
DB 379 GTGCTTATCTGTGTAATATAAAGGACTCAACGCGTGGAAATATCTATCTTCTTAAAC 438
QY 235 CTGGCACTTTCAAACTGTGTTTCTGCTTCCCTGCGGTTCCTGGGCCCATCTACTGACGA 294
DB 439 TTGGCAGTTTCTAACTGTGTTTCTTGTCTTACCTGCCCCCTTCTGGGCTCATGCTG 493
QY 295 CACGGGMAAGCCCTGCAACGGGACCTGTAAAGTTCTTGTGCGACTCCCACTCTCGGGC 354
DB 494 -----RKGCGATCCCATGTGTAAATTTCTCATTTGAGACTGTACTTCTGCGGC 540
QY 355 TTATACAGCAGGAGTGTGTTTCCAAACATCTCTCTCTTGTGCAAGGATACAGGGTGTGTTTC 414
DB 541 CTGTACAGTGAGACATTTTCAATTTGCTTCTGACTGTGCAAGGTACCTTAGTGTGTTTG 600
QY 415 CAAGGGGAC---TGGCTCCATCTTCAACAGAGTGTCTTGTGGTATTGTTGGTGATC 471
DB 601 CACAAGGMAACTTTTCTCAGCCAGGAGGAGGTGCCCTGTGGCATCATTTACAAGTGTG 660
QY 472 CTGGCATGGCCATGCTGCTCTTTTCCCGAGTCTGTGTTTATGAGCTTCGG 531
DB 661 CTGGCATGGTAAACAGCCATTTCTGGCCATTTGCCGTGAATGTTGGTTTATTAACCTCAG 720
QY 532 ATGGAAGACAGAAACACAAAGTGTGCTTTGGCAACCTCACTTCTTGGCAATCGAAGCG 591
DB 721 ATGGAAGACAGAAATACAAAGTGTGATTTAGCAGAACTCCCTTCTCTGCCAGCTGATGAG 780
QY 592 CCCTCTGGAAGTACGTTCTGACGTCAAAATGATCATCTTGTGTTCTGTTTCTCTG 651
DB 781 ACATTCTGGAAGCATTTTCTGACTTTTAAATAATGAACATTTGCTTCTTCTCTCCCTCCTA 840
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; SEQ ID NO 17557
; LENGTH: 14341
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-17557

Query Match      39.1%; Score 423.2; DB 21; Length 14341;
Best Local Similarity 65.2%; Pred. No. 4.6e-131;
Matches 706; Conservative 5; Mismatches 338; Indels 33; Gaps 5;

QY 1 ATGGATAACTACACAGTGGCCCGGAGATGAATATGATGCTCTTAATCTTTAGACGACTAC 60
Db 6892 ATGCCCAATTTCACGCTGGCCACGAGGATGAATATGATGCTCTTAATGAGGTGAA 6948
QY 61 CTGGACAACAGTGGGCGGACCAAGTT-----CCGGCCCCCGAGTTCTCTCCCCCAG 114
Db 6949 CTGGAGAGCATGAGGCGAGCAATGTGACAAGTATGACGCCCGAGCACTCTCAGCCAG 7008
QY 115 CAGGTCTGCAGTCTGCTGCGGGGTGTTGCGGTGCTCTTGGACAACGTCCTGGCG 174
Db 7009 CTGGTGCATCACTGCTCTGCTGCTGTTGTCGTCGTCCTGTCGACAACTCTCTGGTT 7068
QY 175 GTGTTTATCTTGTGAAATACAAAGGACTCAAGAACTCTGGGAAACATCTACTTCTTAAC 234
Db 7069 GTGCTTATCTGTAAATATAAGGACTCAACGCGTGGAAATATCTATCTTCTTAAC 7128
QY 235 CTGGCACTTTCAAACTGTGTTCTGCTTCCCTGCGGTTCTGGGCCCATATCGACGA 294
Db 7129 TTGGCAGTTTCTAACTTGTGTTCTTGTCTTACCTGCGCTTCTGGGCTCATGCTG---- 7183
QY 295 CACGGGGAACCCCTGGCAGCGGACCTGTAAGTTCTTGTGCGACTCCCACTCTCGGCG 354
Db 7184 -----RKGGCGATCCCATGTTGTAAGTTCTCAATGGACTGACTTCTGTTGGCG 7230
QY 355 TTATACAGCAGGTGTTTTCCAACTCTCTCTGTCGCAAGATACAGGGTGTGTTTCC 414
Db 7231 CTGTACAGTGAGACATTTTTCAATGCTTCTGACTGTGCAAGGTACCTAGTGTGTTTG 7290
QY 415 CAAGGGGGAC---TGGCTCCATCTTTCACAGAGTGTCTTGGGTATGTTGGTGATC 471
Db 7291 CACAAGGGMAACTTTTTCTCAGCCAGGAGGAGGTGCTCTGTGGCATATTACAAGTGC 7350
QY 472 CTGGCATGGCCATGCTGCTGCTCTCTTCCCGAGTCTGTGTTTATGAGCCTCGG 531
Db 7351 CTGGCATGGGTAAACGCCATCTTGGCCACTTTCGCTGAATGCTGTTTATAAACCTCAG 7410
QY 532 ATGGAAGACAGAAACACAAAGTGTGCTTTGGCAAACTCCTCACTTTTGCCAATCGAAGCG 591
Db 7411 ATGGAAGACCAGAAATACAAAGTGTGATTTAGCAGAACTCCCTTCTGCCAGCTGATGAG 7470
QY 592 CCCTCTGGAAGTACGTTCTGAGCTCAAAATGATCATCTTGTGACTTGTCTTTCTCTG 651
Db 7471 ACATTTCTGGAAGCATTTCTGACTTTTAAATAATGAACATTTTCGGTCTTGTCTCTCCCTA 7530
QY 652 CTGGTTTTTATATCTGCTGCAGCAACTGAGGAGAGGCGAGAGTTCAGGGAGAGACAG 711
Db 7531 TTTATTTTACATTTCTATGTGCAATGAGAAAACATAAGGTTTACGGAGAGAGG 7590
QY 712 TAGCACTTCAAGCGGCTCTTGTATCAACGGGGGTGTTCTCTTTTGTGTTGGGGCCT 771
Db 7591 TATAGCTTTTCAAGCTTGTGTTTGGCCTAATGTTAGTCTTCTCTGATGTGGGCGCC 7650
QY 772 TACAACATGTGCTTTTCTGCTGCTTCCAGGAACACTTGTCTCTGAGGATGAGAG 831
Db 7651 TACAATATTGCAATTTTCTGCTCACTTTCAAGAAACACTTCTCTGAGTGAAGTCAAG 7710
QY 832 AGCAGCTTACCCTGAGCGCAAGTGTTCAGGTCAACAGCTGTTAGCGACCACTGTC 891
Db 7711 AGCAGCTTACATCTGACAAAAGTGTTCATCACTAATCACTATCGCACCACTGTC 7770
QY 892 TGGCTCAACCGCTGCTCTATTGTTCTTGTGACCGGAAGCCTTTATGAGATACCTTCGC 951
Db 7771 TGCTCAACCCCTCTCTGATGCTTCTTGTGAGGGA---CATTTAGCAAAATACCTCTGC 7827
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QY 952 AGCCTTTTCCCAAGGTGCAATGATATCCCTATCAAAGTAGTGGAGGCTATCAGCAGCG 1011
Db 7828 CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACAAGGC 7887
QY 1012 CTCCCAAGGGAAGGTCTATGCGAGGCCCATTTGAATCTGTACAGCAATTTGCAATCAAAGCAG 1071
Db 7888 ACATCAGGGAAGAACCTGACCATTTCCACGGAAGTGTAACTAGCATCCACCAATGCAA 7947
QY 1072 GA 1073
Db 7948 GA 7949

RESULT 5
US-10-029-386-22780
; Sequence 22780, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 22780
; LENGTH: 1140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO U95626.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.99
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
; OTHER INFORMATION: EST HUMAN HIT: B1834559.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: O97883, EVALUE 2.00e-63
; OTHER INFORMATION: NT HIT: g114736672, EVALUE 0.00e+00
US-10-029-386-22780
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Query Match      39.0%; Score 422; DB 16; Length 1140;
Best Local Similarity 65.5%; Pred. No. 3.1e-131;
Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;

QY 1 ATGGATAACTACACAGTGGCCCGGAGATGAATGATGCTCTTAATCTTAGACGACTAC 60
Db 13 ATGGCAATTTACACGCTGGCACCGAGGATGAATATGATGTCC---TCATAGAGGTGAA 69
QY 61 CTGGACAACAGTGGGCGGACCAAGTT-----CCGGCCCCCGAGTTCCTCTCCCCCAG 114
Db 70 CTGGAGAGCATGAGGCGAGCAATGTGACAAGTATGACGCCAGCACTCTCAGCCAG 129
QY 115 CAGGTCTGCAGTCTGCTGCGCGGTGTTGGGTGGGTCTCTTGGACAACGTCGTGGCG 174
Db 130 CTGGTGCATCACTCTGCTCTGCTGTTGTTGATCGGTGTCCTGGACAATCTCTGGTT 189
QY 175 GTGTTTATCTTGGTGAATACAAAGGACTCAAGAACTCTGGGGAACATCTACTTCTTAAC 234
Db 190 GTGCTTATCTGTGTAATAATAAGGACTCAACGCGTGAATAATATCTATCTTCTTAAC 249
QY 235 CTGGCACTTTCAAACTGTGTTTCTCTGCTTCCCTGCTCCGTTCTGGGCCCATATCTGACGA 294
Db 250 TTGGCAGTTTCTAACTTGTGTTTCTTGTCTTACCTGCTCTCTGGGCTCATGCTG---- 304
QY 295 CACGGGGAAGCCCTGGCAACGGGACCTGTAAAGTTCTTGTGGACTCCTCCTCGGCG 354
Db 305 -----GGGGCGATCCCATGTTGTAATAATCTCAITGGACTGACTTCTGTTGGCG 351
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Qy 355 TTATACAGCAGGAGTGTGTTTCCAAATCCTCTCTCTGTCAGGATACAGGGTGTTC 414
Db 352 CTGTACAGTGAGACATTTTCAATGTCCTTCTGACTGTGCAAGGTACTAGTGTGTTG 411
Qy 415 CAAGGGCGAC---TGGCCTCCATCTTCACGACAGTGTCTTGTGGPATTTGTCGTGCATC 471
Db 412 CACAAGGGCAACTTTTCTCAGCCAGGAGGAGGGTCCCTCTGTGGCATCATTTACAAGTGT 471
Qy 472 CTGGCATGGGCATGGCTACTCGCTCTCTTGTCCCGAGTCTGTGTGTTTATGAGCCTGG 531
Db 472 CTGGCATGGGTAAACAGCAATCTGGCCACTTTCCTGATACGTGGTGTATTAACCTCAG 531
Qy 532 ATGGAAGACAGAAACACAGGTGGCTTTTGGCAAACTCTACTTCTGCCAATCGAAGCG 591
Db 532 ATGGAAGACCAAGAAATACAGGTGTGCAATTTAGCAGAACTCCCTTCTGCCAGCTGATGAG 591
Qy 592 CCGCTCTGGAAGTACGTTCTCAGCTCAAAATGATCATCTTGGTACTTCTTCTCTG 651
Db 592 ACATTCTGGAAGCAATTTCTGACTTTAAAAATGAACATTTCCGGTCTTGTCTCCCTCA 651
Qy 652 CTGGTTTTTATAATCTGCTGCAGGCAACTGAGGAGAGGCGAGAGCTTCAGGGAGAGACAG 711
Db 652 TTTATTTTACATTTCTCTATGTGCAATGAGAAAACATTAAGTTTCAGGGAGCAGAGG 711
Qy 712 TAGCACTCTCAAGCCGCTCTTGTCTATAACGGGCGTGTCTCTTTTGATGTGGCGCT 771
Db 712 TATAGCCTTTTCAAGCTTGTGTTTGGCCATAATGGTAGTCTTCTCTGATGTGGCGCC 771
Qy 772 TACAACACTGTCTTTCTGCTGTCTTTCAGGAACTTGTCTCTCGCTCGCAGGATGAGAG 831
Db 772 TACAATATTCATTTTCTCTGCTGCACTTTTCAAGAACACATTTCTCCCTGAGTGACTGCAAG 831
Qy 832 AGCAGCTACCACTGGAGCGAAGTGTTCAGGTTCACACAGCTGTAGCGACCACTGTC 891
Db 832 AGCAGCTACATCTGGCAAAAGTGTTCATCTACTAACTATCGCCACCACTGTC 891
Qy 892 TGCCTCAACCCGCTGCTCTATTGCTTCTTGACCGGAGGCGCTTTATGAGATACCTTCGC 951
Db 892 TGCATCAACCTCTCTCTGTATGCGTTCCTGATGCGA---CATTTAGCAATACCTCTGC 948
Qy 952 AGCTGTGTCCACCGTGCAATGATATCCCTTATCAAGTAGTGGAGGCTATCAGACGC 1011
Db 949 CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCAAGGC 1008
Qy 1012 CTTCAAGGGAAGTCTAGGCGAGGCCAATGAACTGTACACAAATTTGCATCAAGGCGAG 1071
Db 1009 ACATCGAGGGAAGAACCTGACCATTCACCGAAGTGTAAACTAGCATCCACCAATGCA 1068
Qy 1072 GA 1073
Db 1069 GA 1070
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RESULT 6

US-10-223-085-15

; Sequence 15, Application US/10223085

; Publication No. US20030100497A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Masters, Scot A.

; APPLICANT: Pan, James

; APPLICANT: Stephan, Jean-Philippe F.

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Ye, Weilan

```
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C10
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; CURRENT APPLICATION NUMBER: US/10/223,085

; CURRENT FILING DATE: 2002-08-16

; PRIOR APPLICATION NUMBER: US 10/081,056

; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: US 60/213,637

; PRIOR FILING DATE: 2000-06-23

; PRIOR APPLICATION NUMBER: US 60/219,556

; PRIOR FILING DATE: 2000-07-20

; PRIOR APPLICATION NUMBER: US 60/220,624

; PRIOR FILING DATE: 2000-07-25

; PRIOR APPLICATION NUMBER: US 60/220,664

; PRIOR FILING DATE: 2000-07-25

; PRIOR APPLICATION NUMBER: PCT/US00/20710

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: US 60/222,695

; PRIOR FILING DATE: 2000-08-02

; PRIOR APPLICATION NUMBER: US 09/643,657

; PRIOR FILING DATE: 2000-08-17

; PRIOR APPLICATION NUMBER: PCT/US00/23522

; PRIOR FILING DATE: 2000-08-23

; PRIOR APPLICATION NUMBER: PCT/US00/23328

; PRIOR FILING DATE: 2000-08-24

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 383

; SEQ ID NO 15

; LENGTH: 1475

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-223-085-15

Query Match 39.0%; Score 422; DB 15; Length 1475;

Best Local Similarity 65.5%; Pred. No. 3.5e-131;

Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;

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Qy 1 ATGGATAACTACACAGTGGCCCCCGACGATGAATATGATGTCTTAATCTTAGACGACTAC 60
Db 29 ATGGCCAATTACACGCTGGCCACGAGAGATGAATATGATGTCC---TCATAGAAGGTCAA 85
Qy 61 CTGGACAAAGTGGGCGGACCAAGTT-----CGGGCCCCGAGTTCTCTCCCCCAG 114
Db 86 CTGGAGAGCGATGAGGCGAGAGCAATGTGCAAGATATGACGCCCGAGGCACTCTCAGCCAG 145
Qy 115 CAGGTGTCAGTTCCTGCGCGGTGTTGCGGTGGTCTCTTGGACAAGCTGCTGCGG 174
Db 146 CTGGTGCCATCCTCTGCTGTGTTGTGATCGGTGTCCTGGACAATCTCTCTGTT 205
Qy 175 GTGTTATCTTGTGAAATACAAAGGACTCAAGAAATCTGGGGAACATCTACTTCTTAAC 234
Db 206 GTGCTTATCTGTGTAATAATAAAGGACTCAACGCGTGGAAATAATCTATCTTAAC 265
Qy 235 CTGGCACTTTCAACCTGTGTTTCTGTCCTCCCTCGGTTCTGGGCCCATCTGCGACA 294
Db 266 TTGGCAGTTTCTAACTTGTGTTCTTGTACCTGCGCTTCTGGGCTCATGCTG----- 320
Qy 295 CACGGGGAAGCCCTGGCAACGGGACCTGTAAAGTCTTGTGCGACTCCACTCTCGGGC 354
Db 321 -----GGGGCGATCCCATGTGTAAATAATCTCATTTGGACTGTACTTCTGTTGG 367
Qy 355 TTATACAGCAGGTGTTTTTCCAAACATCTCTCTCTGTGCAAGGATACAGGGTGTTC 414
Db 368 CTGTACAGTGAGACATTTTTCATTTGCTTCTGACTGTGCAAGGATACCTAGTGTGTTG 427
Qy 415 CAAGGGCGAC---TGGCCTCCATCTTCACGACAGTGTCTGTGTGTTATTTGTCGTGCATC 471
Db 428 CACAAGGGCAACTTTTTTCTCAGCCAGGAGGAGGGTGGCTGTGGCATCATTTACAAGTGC 487
Qy 472 CTGGCATGGGCCATGGCTACTGCGCTCTCTTTGCCCCGAGTCTGTGTTTATGAGCCTCG 531
Db 488 CTGGCATGGGTAAACAGCCATTTCTGGCCACTTTCTGCTGAATACAGTGGTGTATTAACCTCAG 547
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Qy	532	ATGGAAGACAGAAACACAAAGTGTGCGCTTTGGCGAAACCTCACTCTTTGGCAATCGAAGCG	591
Db	548	ATGGAAGACAGAAATACAAAGTGTGCAATTTAGCAGAACTCCCTTCTCGCCAGCTGATGAG	607
Qy	592	CCGCTCTGGAGTAGTCTTGACGTCAAAATGATCATCTGGTACCTTGTCTTTTCCNCTCG	651
Db	608	ACATTCGGAGACATTTTCTGACTTTAAAATAGAACATTTGCGTTCCTTGCTCCCCCTA	667
Qy	652	CTGGTTTTTAAATCTGCTGCAGGCAACTGAGGAGAAAGCAGAGCTTTCAGGAGAGACAG	711
Db	668	TTTATTTTTTACATTTCTATGTGCAAAATGAGAAACACATAAGGTTTCAGGGAGCAGAGG	727
Qy	712	TACGACCTCCACAAAGCCGGCTCTTGTCATAAACGGGCGTGTCTCTTTTGATGTGGGCGCCT	771
Db	728	TATAGCCCTTTTCAAGCTTGTTTTTGGCCATAATGGTAGTCTCTCTCTTGATGTGGGCGCCC	787
Qy	772	TACAACTGTGCTTTTCTGTGCTGCTTTCCAGGAACACTTGTCCCTGCAGGATGAGAAG	831
Db	788	TACANTATTTGATTTTTTCTGTGCACCTTTCAAGAACACTTCTCCCTGAGTGACTGCNAG	847
Qy	832	AGCAGCTACCACTCGGACGCAAGTGTTTCAGGTCAACAGCTGGTAGCGACCAACCCTATGC	891
Db	848	AGCAGCTACAATCTGGACAAAGTGTTACATCACTAACTCATCGCCACCCCACTGC	907
Qy	892	TGCGTCAACCGCGTGCTCTATTTCGTTCTTGACCGGAAGCGCTTTATGAGATACCTTCGC	951
Db	908	TGCATCAACCCCTCTCTGTATGCGTCTTCTTGATGGGA---CATTTAGCAAAATACCTCTGC	964
Qy	952	AGCCTGTTCCACCGTGCAATGATATCCCTATCAAAGTAGTGGAGGCTATCAGCAAGCG	1011
Db	965	CGCTGTTTTCCATCTCGGTAGTAAACCCCACTTCAACCCAGGGGGAGTCTGCACAAGGC	1024
Qy	1012	CCTCCAAGGAAGGTCTATGGCAGCGCCATTTGAATCTGTACAGCAATTTGTCATCAAAGGCAG	1071
Db	1025	ACATCGAGGGAGAACCTGACCATTCACCGGAAGTGTAAACTAGCATCCACCAATGCAA	1084
Qy	1072	GA	1073
Db	1085	GA	1086

RESULT 7

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US-10-223-084-15
Sequence 15, Application US/10/223084
Publication No. US20030105011A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austen L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, James
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Williams, P.Mickey
APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235PLC5
CURRENT APPLICATION NUMBER: US 10/223,084
CURRENT FILING DATE: 2002-08-16
PRIORITY APPLICATION NUMBER: US 10/081,056
PRIORITY FILING DATE: 2002-02-20
PRIORITY APPLICATION NUMBER: US 60/213,637
PRIORITY FILING DATE: 2000-06-23
PRIORITY APPLICATION NUMBER: US 60/219,556
PRIORITY FILING DATE: 2000-07-20
PRIORITY APPLICATION NUMBER: US 60/220,624

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QY 892 TGCGTCAACCGGTGCTCTATTTGCTTCTTGACGGAGGCGCTTTATGAGATACCTTCGC 951
DB 908 TGCATCAACCTCTCTGATGCGTTTCTTGATGGGA---CATTTAGCAAAATACCTCTGC 964
QY 952 AGCTGTTCCTCAGGTGCAATGATATCCCTATCAAAAGTAGTGGAGGCTATCAGCAAGCG 1011
DB 965 CGCTGTTTCATCTGCGTAGTAACACCCCACTTCACCCAGGGGCGAGTCTGCACAAGGC 1024
QY 1012 CTCCAAAGGAAGGTCTAGCAGGCGCCATTTGAATCTGTACAGCAATTTGCAATCAAAAGCAG 1071
DB 1025 ACATCGAGGAAGAACCTGACCATTCACCGAAGTGTAAACTAGCATCCCAACCAATGCAA 1084
QY 1072 GA 1073
DB 1085 GA 1086

RESULT 9

US-10-223-090-15
; Sequence 15, Application US/10223090
; Publication No. US20030105013A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: F235P1C2
; CURRENT APPLICATION NUMBER: US/10/223,090
; CURRENT FILING DATE: 2002-08-16
; PRIORITY APPLICATION NUMBER: US 10/081,056
; PRIORITY FILING DATE: 2002-02-20
; PRIORITY APPLICATION NUMBER: US 60/213,637
; PRIORITY FILING DATE: 2000-06-23
; PRIORITY APPLICATION NUMBER: US 60/219,556
; PRIORITY FILING DATE: 2000-07-20
; PRIORITY APPLICATION NUMBER: US 60/220,624
; PRIORITY FILING DATE: 2000-07-25
; PRIORITY APPLICATION NUMBER: US 60/220,664
; PRIORITY FILING DATE: 2000-07-28
; PRIORITY APPLICATION NUMBER: PCT/US00/20710
; PRIORITY FILING DATE: 2000-07-28
; PRIORITY APPLICATION NUMBER: US 60/222,695
; PRIORITY FILING DATE: 2000-08-02
; PRIORITY APPLICATION NUMBER: US 09/643,657
; PRIORITY FILING DATE: 2000-08-17
; PRIORITY APPLICATION NUMBER: PCT/US00/23522
; PRIORITY FILING DATE: 2000-08-23
; PRIORITY APPLICATION NUMBER: PCT/US00/23328
; PRIORITY FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-223-090-15

Query Match 39.0%; Score 422; DB 15; Length 1475;
Best Local Similarity 65.5%; Pred. No. 3.5e-131;
Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;

QY 1 ATGGATAACTACACAGTGGCCCGGACGATGAATATGATGTCTTAATCTTAGACGACTAC 60
DB 29 ATGGCCAATTAACACGCTGGCACGAGGATGAATATGATGTCC---TCATAGAGGTGAA 85
QY 61 CTGGCAACAAGTGGGCGGACCAAGTT-----CGGGCCCCGAGTTCCTCTCCCCCAG 114
DB 86 CTGGAGAGCATGAGGACAGACGCAATGTGACAGTATGACGCCAGGCACTCTCAGGCCAG 145
QY 115 CAGGTCTCGAGTTCCTGCTGCGGCTGTTTGGGTGGGTCTCTTGGACAACAGTGTCTGGCG 174
DB 146 CTGGTGCCATCACTCTGCTCTGCTGTGTTTGTGATCGGTGCTGCGACAAATCTCTCTGGTT 205
QY 175 GTGTTTATCTTGTGTAATAACAAAGGACTCAAGAAATCTGGGGAACATCTACTTCTTAAAC 234
DB 206 GTGCTTATCTGTGTAATAATAAAGGACTCAACGGGTGAAATATATCTATCTTCTTAAAC 265
QY 235 CTGGCACTTTCAAAACCTGTGTTTCTTGCTTCCCTGCGCTTCTGGGCCCATACTATCGAGCA 294
DB 266 TTGGCAGTTTCTAACTTGTGTTTCTTGCTTACCCTGCGCTTCTGCGCTCATGCTG---- 320
QY 295 CACGGGAAAAGCCCTGCGAAACGGGACCTGTAAAGTTCTTGTGCGGACTCACTCTCTGGGC 354
DB 321 -----GGGGCGATCCCATGTGTAAATTTCTCATTTGGAAGTACTTCTGTTGGGC 367
QY 355 TTATACAGCGAGTGTGTTTCCCAACATCTCTCTTGTGCAAGGATACAGGGTGTGTTTCC 414
DB 428 CACAAGGGCAACTTTTCTCAGCCAGGAGGAGGGTGCCTGTGGCATATTACAAGTGTG 487
QY 472 CTGGCATGGGCCATGCGTACTGCGCTCTCTTGGCCGAGTCTGTGTGTTTATGAGCTCGG 531
DB 488 CTGGCATGGGTAAACAGCCATTCTGGCCACTTGTGGCTGAATACGTGGTTTATATAACCTCAG 547
QY 532 ATGGAAGACAGAAACACAAAGTGTGCTTTGGCAACCTCCTCTTGGCAATCGAAGCG 591
DB 548 ATGGAAGACAGAAATACAAAGTGTGCAATTTAGCAGAACTCCCTTCTGCCAGCTGATGAG 607
QY 592 CGCTCTGGAAGTACGTTCTGACGTCAAAAATGATCATCTTGGTACTTGTCTTCTCTG 651
DB 608 ACATCTGGAAGCATTTTCTGACTTTTAAATAATGAAACATTTGCGTTCTTGTCTCTCCCTA 667
QY 652 CTGGTTTTTATATCTGCTGCGAGGCAACTGAGGAGGAGCAGAGCTTCAAGGAGACAG 711
DB 668 TTTATTTTACATTTCTCTATGTGCAAAATGAGAAAAACAATAAGGTTCAAGGAGCAGAGG 727
QY 712 TAGCACTCCAAAGCGGCTCTTGTCAATAACGGGGTGTGTTCTTTTGTGATGCGGCGCCT 771
DB 728 TATAGCTTTTCAAGCTTGTGTTTGGCAATATGGTAGTCTTCTTCTGATGTGGGCGCC 787
QY 772 TACAACACTGTCTTTCTGCTGTGCTTTCCAGGAACACTTGTCTCTGAGGATGAGAAG 831
DB 788 TACAATATTGCAATTTTCTGCTCCACTTTCAAAGAACACTTCTCTCTGAGTGAAGCAAG 847
QY 832 AGCAGTACCACTGACGCAAGTGTTCAGTTCACAGCTGGTAGGAGCACCACCTGC 891
DB 848 AGCAGCTACAATCTGGACAAAAGTGTTCATCATCACTATAAACTCATGCCACCACTGC 907
QY 892 TGGCTCAACCCGCTGCTCTATTGCTTCTTGTACCGGAAGGCTTTTATGAGATACCTTCGC 951
DB 908 TGCATCAACCTCTCTCTGTATGCGTTTCTTGTATGGGA---CATTTAGCAAAATACCTCTGC 964
QY 952 AGCTGTTCCCAAGGTCGAATGATATCCCTATCAAAAGTAGTGGAGGCTATCAGCAAGCG 1011
DB 965 CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCAAGGC 1024
QY 1012 CTCCAAAGGAGGTCACTGCGAGGCGCAATTGAACTGTACAGCAATTTGATCAAAAGCAG 1071
DB 1025 ACATCGAGGAAGAACCTGACCATTCACCGAAGTGTAAACTAGCATCCCAACCAATGCAA 1084


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Db 368 CTGTACAGTGAACAATTTTCAATGCTCTGACTGTGCAAAAGGTACCTAGTGTGTTTG 427
Qy 415 CAAGGGCGAC---TGGGCTCCATCTTCACGACAGTGTCTTGTGGTAFTTGTGGTGCAATC 471
Db 428 CACAAGGGCAACTTTTCTCAGCCAGGAGGAGGTGCCCTGTGGCATCAATACAAAGTGC 487
Qy 472 CTGGCATGGGCATGGCTACTCGGCTCTCTTGGCCGAGTCTGTGTTTATGAGCCTCGG 531
Db 488 CTGGCATGGGTAAACAGCACTTCCTGGCCACTTTCCTGGAATACGGTGGTTTATAAACCTCAG 547
Qy 532 ATGGAAGACAGAAACACAAGTGTGCCCTTTTGGCAAACTCACTTCTTGCCAAATCGAAGCG 591
Db 548 ATGGAAGACAGAAATACAAAGTGTGCATTTAGCNGAACTCCCTCTCGCCAGCTGATGAG 607
Qy 592 CCGCTCTGGAAGTACGTTCTGACGTGCAAAATGATCAATCTTGGTACTTGTCTTTTCTCTG 651
Db 608 ACATTTCTGGAAGCAATTTCTGACTTTAAAAATGAACATTTTCGGTTCCTTGTCTCCGCCCTA 667
Qy 652 CTGGTTTTTAAATCTCTCGACGCACTGAGGAGAGGAGAGTCTTCAGGGAGAGACAG 711
Db 668 TTTATTTTAACTTCTCTATGTGCAATAGAAAAACATAAGGTTTCAGGGAGCAGAGG 727
Qy 712 TAGCACTCCACAGCGCGCTCTGTGATTAACGGGGGTGTTCTTTTGTGATGTGGGGCCT 771
Db 728 TATAGCCTTTTCAAGCTTGTGTTTGGCAATATGATGTCTCTCTCTGATGTGGGGCCC 787
Qy 772 TACAACACTGTGCTTTTCTGCTGTCTTCCAGAAACATTTGCTCCCTGACGAGTAGAAG 831
Db 788 TACAATATTGCAATTTTCTGTCTCCTTTTCAAGAACACATTTCTCCCTGAGTGACTGCAAG 847
Qy 832 AGAGCTACCACTGGAGCGAAGTGTTCAGTCTACAGCTGTGTAGGACCACTGCTGC 891
Db 848 AGAGCTACCAATCTGGACAAAGGTGTTCACTCACTAAACTCATCGCCACCACTGCTGC 907
Qy 892 TGCGTCAACCCGCTGCTCTATTTGCTTCTTGACCGGAAGGCTTTTATGATACCTTGC 951
Db 908 TGCAATCAACCTCTCTGATGCTGTTCTTGTATGGGA---CATTTAGCAATACCTTGC 964
Qy 952 AGCTGTTCCTCCAGGTGCAATGATATCCCTATCAAAAGTATGAGGAGCTATCAGCAAGC 1011
Db 965 CGCTGTTTCCATCTGCGTAGTAAACACCCCACTTCAACCCAGGGGGCAGTCTGCACAAAGC 1024
Qy 1012 CTTCCAGGGAAGTCAATGACGAGCCCAATTTGAATGTACAGCAATTTGCATCAAGGCGAG 1071
Db 1025 ACATCGAGGGAAGAACCTGACCAATTCACCGAAAGTGTAAACTAGCATCCCAATGCAA 1084
Qy 1072 GA 1073
Db 1085 GA 1086
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RESULT 11
US-10-223-083-15

; Sequence 15, Application US/10223083
; Publication No. US2003011912A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS

; FILE REFERENCE: P3235P1C8

; CURRENT APPLICATION NUMBER: US/10/223,083

; CURRENT FILING DATE: 2002-08-16

; PRIOR APPLICATION NUMBER: US 10/081,056

; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: US 60/213,637

; PRIOR FILING DATE: 2000-06-23

; PRIOR APPLICATION NUMBER: US 60/219,556

; PRIOR FILING DATE: 2000-07-20

; PRIOR APPLICATION NUMBER: US 60/220,624

; PRIOR FILING DATE: 2000-07-25

; PRIOR APPLICATION NUMBER: US 60/220,664

; PRIOR FILING DATE: 2000-07-25

; PRIOR APPLICATION NUMBER: PCT/US00/20710

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: US 60/222,695

; PRIOR FILING DATE: 2000-08-02

; PRIOR APPLICATION NUMBER: US 09/643,657

; PRIOR FILING DATE: 2000-08-17

; PRIOR APPLICATION NUMBER: PCT/US00/23522

; PRIOR FILING DATE: 2000-08-23

; PRIOR APPLICATION NUMBER: PCT/US00/23328

; PRIOR FILING DATE: 2000-08-24

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 383

; SEQ ID NO 15

; LENGTH: 1475

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-10-223-083-15

Query Match 39.0%; Score 422; DB 15; Length 1475;

Best Local Similarity 65.5%; Pred. No. 3.5e-131;

Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;

Qy 1 ATGGATAACTACACAGTGGCCCGGACGATGAATATGATGTCTTAATCTTAGACGACTAC 60

Db 29 ATGGCCAAATACACGCTGGCACACAGGATGAATATGATGTCC---TCATAGAGGTGAA 85

Qy 61 CTGGCAACACAGTGGGCGGACCAAGTT-----CGGGCCCCGAGTTCCTCTCCCCCAG 114

Db 86 CTGGAGAGCGATGAGGACAGCAATGTGACAAAGTATGACGCCAGGCACTCTCAGCCAG 145

Qy 115 CAGGTGCTCGAGTCTGTCGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGT 174

Db 146 CTGGTCCATCACTCTGCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 205

Qy 175 GTGTTTATCTGTGAAATACAAAGGACTCAAGAATCTGGGGAACATCTACTTCTTAAAC 234

Db 206 GTGCTTATCTGTGAAATATAAAGGACTCAAAAGGCTGGAATAATCTATCTTCTTAAAC 265

Qy 235 CTGGCACTTTCAAACTGTGTTTCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 294

Db 266 TTGGCAGTTTCTAATCTGTGTTTCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTG 320

Qy 295 CAGGGGAAAGCCCTGGCAACGGGACCTGTAAAGTCTTGTGCGGACTCCTCCTCGGC 354

Db 321 -----GGGGCGATCCCATGTGTAAAAATTCATTTGGAATGCTGCTGCTGCTG 367

Qy 355 TTATACAGCGAGTGTGTTTTCACCAATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 414

Db 368 CTGTACAGTGAACAATTTTTCATTTGCTTCTGACCTGTGCTGCTGCTGCTGCTGCTG 427

Qy 415 CAAAGGCGAC---TGGCCTTCCATCTTCAGCAGAGTGTCTTGTGGTATTTGTGCTGCATC 471

Db 428 CACAAGGGCAACTTTTCTCAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 487

Qy 472 CTGGCATGGGCCATGGCTACTGCGCTCTCTTTGCGCGAGTCTGTGTTTATGAGCCTCG 531

Db 488 CTGGCATGGGTAAACAGCCACTTCTGGCCACTTCTGGCCACTGATGCTGCTGCTGCTG 547

Qy 532 ATGGAAGACAGAAACACAAGTGTGCTTTTGGCAAACTCACTTCTTGTGCAATCGAAGCG 591

Db 548 ATGAAGACCAAGAAATACAAGTGTGCAATTTAGCAGAACTCCCTTCTGCCAGCTGATGAG 607
Qy 592 CCGCTCTGGAAGTAGTCTGACGTCAAAAATGATCATCTTGGTACTTGTCTTTCTCTG 651
Db 608 ACATTCTGGAAGCAATTTCTGACTTTAAAAATGAACATTTCCGGTCTTGTCTCCCTC 667
Qy 652 CTGGTTTTTATAATCTGCTGACGAGCACTGAGGAGAGGAGAGCTTCAGGAGAGACAG 711
Db 668 TTTATTTTACATTTCTATGTGCAATGAGAAAAACACTAAGTTTCAGGAGACAGAG 727
Qy 712 TACGACCTCCAAAGCGCGCTTGTGTAACAGGCGGTGTTCTTTTGTATGTGGCGCT 771
Db 728 TATAGCCCTTTTCAAGCTTGTGTTTGGCCATAATGGTAGTCTTCTCTGATGTGGCGGCC 787
Qy 772 TACAACACTGTGCTTCTCTGCTGCTTCTCCAGGAGCACTTGTCCCTGCAGATGAGAG 831
Db 788 TACAATATGCAATTTTCTGTCACATTTTCAAGAACACATTTCTCCCTGAGTGACTGCAAG 847
Qy 832 AGCAGCTACCACTGGAGCGCAAGTGTTCAGGTACACAGCTGTGAGCGACCACTGTC 891
Db 848 AGCAGCTACATCTGGACAAAAGTGTTCACATCACTAACTCATCGCCACCACTGTC 907
Qy 892 TGGTCAACCGCTGCTCTATTGCTTCTGACCGGAGGCGCTTTATGAGATACCTTGC 951
Db 908 TGCATCAACCTCTCTGATGCGTTTCTGATGGGA---CATTTAGCAATACCTCTGC 964
Qy 952 AGCTGTGTCCACCGTGCAATGATATCCCTTATCAAGTAGTGGAGGCTATCAGCAAGC 1011
Db 965 CGTGTGTTCATCTGCGTAGTAACACCCCACTTCAACCCAGGCGGAGCTGCAACAAGC 1024
Qy 1012 CCTCAAGGGAAGTCAAGGAGGCGCCATTTGAACTGTACAGCAATTTGCAATCAAGGAGC 1071
Db 1025 ACATCGAGGAGAACCTGACCATTCACCGAAGTGTAACTAGCATCCCAATGCA 1084
Qy 1072 GA 1073
Db 1085 GA 1086

RESULT 12

US-10-223-089-15
; Sequence 15, Application US/10223089
; Publication No. US20030125521A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235PL9
; CURRENT APPLICATION NUMBER: US/10/223,089
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25

Query Match 39.0%; Score 422; DB 15; Length 1475;
Best Local Similarity 65.5%; Pred. No. 3.5e-131;
Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;
US-10-223-089-15

Qy 1 ATGGAATAACTACACAGTGGCCCGGACGATGAATATGATGCTTAATCTTAGACGACTAC 60
Db 29 ATGSCCAATTACACGCTGGCACACAGAGATATGATGTCC---TCATAGAAGTGAA 85
Qy 61 CTGGAACAAGTGGCGCGGACCAAGTT-----CCGGCCCCGAGTTCTCTCCCCCAG 114
Db 86 CTGGAGAGCGATGAGGCGAGACATGTGACAAGATGACGCCAGGCACTCTCAGCCCCAG 145
Qy 115 CAGTGTCTGACGTCTCTCGCGGTGTTTCGGTGTCTTGGCAACAGTGTCTGCGG 174
Db 146 CTGTGCGCATCACTCTCTCTGCTGTGTTGTATCGTGTCTTGGACATCTCTCTGTT 205
Qy 175 GTGTTATCTTGGTGAATAACAAGGACTCAAGAATCTGGGGAACATCTACTTCTTAAC 234
Db 206 GTGCTTATCTGTTAAATATAAAGGACTCAACCGCTGGAAATATCTATCTCTTAAC 265
Qy 235 CTGGCACTTTCAAACTGTGTTCTCTCTCCCTCGCGGTCTCGGGCCATCTGTCAGCA 294
Db 266 TTGGCAGTTTCTAACTTGTGTTCTTGTCTTACCCTGCGCTTCTGGGCTCATGCTG- 320
Qy 295 CACGGGGAAGCCCTGGCAACGGGACCTGTAAGTCTTGTGCGACCTCCACTCTCGGGC 354
Db 321 -----GGGCGGATCCCATGTGTGTAATAATCTCATTTGGACTGTACTTGTGGC 367
Qy 355 TTATACAGCGAGTGTGTTTCCAAACATCTCTCTCTGTCAGAGGATACAGGGTGTGTTCC 414
Db 368 CTGTACAGTGAGACATTTTTCATTTGCTTCTGACTGTGCAAGGTACCTAGTGTGTTG 427
Qy 415 CAAGGGCGAC---TGGCTCATCTTCACGACAGTGTCTGTGTGTATTTGTGCGTGCATC 471
Db 428 CACAAGGGCAACTTTTCTCAGCCAGGAGGAGGTGCGCTGTGGCATCATTTACAAAGTGT 487
Qy 472 CTGCGATGGGCCATGGCTACTGCGCTCTCTTTCGCCGAGTCTGTGTTTATGAGCTCGG 531
Db 488 CTGGCATGGGTAAACAGCCATTTCTGGCCACTTTGCTGTAATACGTTGTTTAAACCTCAG 547
Qy 532 ATGGAAGACAGAAACACAAAGTGTGCTTTGGCAAACTCTCACTTTCTTGGCAATCGAAGCG 591
Db 548 ATGGAAGACAGAAATACAAAGTGTGCAATTTAGCAGAACTCCCTTCTCGCCAGCTGATGAG 607
Qy 592 CCGCTCTGGAAGTAGTCTTGTGAGTCAAAAATGATCATCTTGGTACTTGTCTTTCTCTG 651
Db 608 ACATTTCTGGAAGCAATTTCTGACTTTTAAAAATGAACATTTCCGGTCTTGTCTCCCTC 667
Qy 652 CTGGTTTTTATAATCTGCTCAGCACTGAGGAGAGGAGAGCTTTCAGGAGAGACAG 711
Db 668 TTTATTTTACATTTCTCTATGTGCAATGAGAAAAACACTAAGTTTCAGGAGACAGAG 727
Qy 712 TACGACCTCCAAAGCGCGCTCTTGTGTAACAGGCGGTGTTCTCTTTTGTGAGTGTGGCGCCT 771

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Db 728 TATAGCCTTTTCAAGCTGTGTTTTGGCCATAATGGTAGTCTTCCTTCTGATGTGGGCGCC 787
QY 772 TACAACAACCTGTGCTTTTCCCTGTCTGCTTTCCAGAACACCTTGTCCCTGCAGGATGAGAAG 831
Db 788 TACAATATTTGCAATTTTCTGTCTTCCACTTTCAGAGAACACTTCTCCCTGAGTGACTGCAAG 847
QY 832 AGCAGCTACCACTTGCAGCAAGTGTTCAGGTTCACAGCTGCAGGATGAGGACCACTGCTGC 891
Db 848 AGCAGCTACAATCTGGACAAAGTGTTCACATCACTAAATCTATCGCCACCACTGCTGC 907
QY 892 TCGCTCAACCCGCTGTCTATTTGCTTTTACCGGAAGCCCTTTATGAGATACCTTCGC 951
Db 908 TGATCAACCCCTCTCTGTATGGTTCCTGTATGGGA---CATTTAGCAATACCTCTGC 964
QY 952 AGCCTGTTCACGGTGCATATATCCCTATCAAAAGTAGTGGAGGCTATCAGCAAGCG 1011
Db 965 CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGGCAGTCTGCACAAGGC 1024
QY 1012 CTCCAAAGGAAGTCAATGCAAGCCCATTTGAAGTGTACAGCAATTTGCAATCAAGGCAG 1071
Db 1025 ACATCGAGGAAGAACCTGACCAATTCACCGAAGTGTAAACTAGCATCCACCAATGCAA 1084
QY 1072 GA 1073
Db 1085 GA 1086
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RESULT 13

US-10-223-081-15

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; Sequence 15, Application US/10223081
; Publication No. US20030186866A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: F3235P1C7
; CURRENT APPLICATION NUMBER: US/10/223,081
; PRIOR FILING DATE: 2002-08-16
; PRIOR FILING DATE: 2002-08-16
; PRIOR FILING DATE: 2002-02-20
; PRIOR FILING DATE: 2002-02-20
; PRIOR FILING DATE: 2000-06-23
; PRIOR FILING DATE: 2000-07-20
; PRIOR FILING DATE: 2000-07-20
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-07-28
; PRIOR FILING DATE: 2000-07-28
; PRIOR FILING DATE: 2000-07-28
; PRIOR FILING DATE: 2000-08-02
; PRIOR FILING DATE: 2000-08-02
; PRIOR FILING DATE: 2000-08-17
; PRIOR FILING DATE: 2000-08-17
; PRIOR FILING DATE: 2000-08-23
; PRIOR FILING DATE: 2000-08-23
; PRIOR FILING DATE: 2000-08-24
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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-223-081-15

Query Match 39.0%; Score 422; DB 16; Length 1475;
Best Local Similarity 65.5%; Pred. No. 3.5e-131;
Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;

QY 1 ATGGATAAATACACAGTGGGCGGACGATGAATATGATGTCTTAATCTTAGACGACTAC 60
Db 29 ATGGCCAAATTAACACGCTGGCACCAGAGGATGAATATGATGTCC---TCATAGAAGTGAA 85
QY 61 CTGGACAACAGTGGGCGGACCAAGTT-----CGGCGCCCGGAGTTCCTCTCCCCCAG 114
Db 86 CTGGAGAGCGATGAGGCGAGAGCAATGTGACAAGTATGACGCCGAGCACTCTCAGCCAG 145
QY 115 CAGGTCTGAGTTCCTGTCGCGGTGTTTGGGTGGTCTCTTGGACAACGTCGTGGCG 174
Db 146 CTGGTCCCATCACTCTGCTCTGCTGTGTTTGTGATCGGTCTCTGGACAATCTCTGGTT 205
QY 175 GTGTTTATCTTGGTGAATACAAAGGACTCAAGAATCTGGGGAACATCTACTTCTTAAAC 234
Db 206 GTGCTTATCTGTGTAATAATATAAGGACTCAAGCGGTGGAATAATATCTATCTTAAAC 265
QY 235 CTGGCACTTTCAAACTGTGTTTCTGCTTCCCTGCGGTTCTTGGGCCCATATCTGACGA 294
Db 266 TTGGCAGTTTCTAACTGTGTTTCTGCTTACCTGCGCTTCTTGGGCTCATGCTG---- 320
QY 295 CAGGGGAAGCCCTGGCAACGGGACCTGTAAAGTTCCTTGTGGACTCACTCTCGGGC 354
Db 321 -----GGGCGCATCCCATGTGTAAAAATCTCATTTGGACTTACTTTCGTGGC 367
QY 355 TTATACAGCGAGTGTGTTTCCCAACATCTCTCTGTCGCAAGATACAGGTTGTTTCC 414
Db 368 CTGTACAGTGAACATTTTCAATTCCTTCTGACTGTGCAAGGTACCTAGTGTGTTTG 427
QY 415 CAAGGCGGAC---TGCCCTCCATCTTTCAGCAGAGTGTCTTGTGGTATTTGTCGTGCATC 471
Db 428 CACAAGGCAACTTTTCTCAGCCAGGAGGAGTGCCTGTGGCATATTACAAGTGTG 487
QY 472 CTGGCATGGCCATGCTACTGCGCTCTCTTTCGCGAGTCTGTGTGTTTATGAGCTCG 531
Db 488 CTGGCATGGGTAAACAGCCATTTCTGGCCACTTTTGGCTGAATACGTGGTTTATAAACCTCAG 547
QY 532 ATGGAAGACAGAAACACAGTGTGCTTTGGCAACCTCACATCTTTGCAATCGAAGCG 591
Db 548 ATGGAAGACAGAAATACAGTGTGCAATTTAGCAGAACTCCCTTCTGCCAGCTGATGAG 607
QY 592 CGCTCTGGAAGTACGTTCTGAGCTCAAAATATGATCATCTTGGTACTTGTCTTCTCTG 651
Db 608 ACATCTGGAAGCATTTTCTGACTTTTAAATAATGAACATTTTCGGTCTTGTCTCTCCCTA 667
QY 652 CTGGTTTTTATATCTGCTGAGGCAACTGAGAGAGAGGAGAGGAGGAGGAGGAGGAG 711
Db 668 TTTATTTTACATTTCTCTATGTGCAAAATGAGAAAAACACTAAGGTTTCAGGAGGAGGAG 727
QY 712 TAGGACTCCACAAGCGGCTCTTGTCAATAACGGGCTGTCTCTTGTGATGTGGGCGCT 771
Db 728 TATAGCTTTTCAAGCTGTGTTTGGCAATATGTTAGTCTTCTCTGATGTGGGCGCC 787
QY 772 TACAACACTGTGCTTTTCTGCTGCTTTCCAGGAACACTTGTCTCTGCAAGATGAGAAG 831
Db 788 TACAATATTTGCAATTTTCTGCTCCACTTTCAAAAGAACACTTCTCTCTGAGTGACTGCAAG 847
QY 832 AGCAGCTACCACTGCAAGGCAAGTGTTCAGGTCAACAGCTGTGAGGACCACTGCTGC 891
Db 848 AGCAGCTACAATCTGGACAAAGTGTTCACATCACTAAATCTATCGCCACCACTGCTGC 907
QY 892 TCGGTCAACCCGCTGTCTATTTGCTTTTACCGGAAGCCCTTTATGAGATACCTTCGC 951
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Db 908 TGCATCAACCCCTCTCTGATGCGTTTCTGTATGGGA---CATTTAGCAAAATACCTCTGC 964
Qy 952 AGCCTGTTCCCAAGGTGCAATGATATCCCTATCAAGTAGTGGAGGTATCAGCAAGG 1011
Db 965 CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGGAGTCTGCAAGGC 1024
Qy 1012 CCTCAAGGGAAGGTGATGCGAGGCCCATTTGAACTGTACAGCAATTTGCATCAAAAGGCAG 1071
Db 1025 ACATCGAGGGAAGAACCTGACCATTCACCGAAGTGTAACTAGCATCCACCAATGCAA 1084
Qy 1072 GA 1073
Db 1085 GA 1086

RESULT 14

US-10-223-082-15
; Sequence 15, Application US/10223082
; Publication No. US20030191059A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Wellan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C3
; CURRENT APPLICATION NUMBER: US/10/223,082
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-223-082-15

Query Match 39.0%; Score 422; DB 16; Length 1475;
Best Local Similarity 65.5%; Pred. No. 3.5e-131;
Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;

Qy 1 ATGGAATAACTACACAGTGGCCCGGACGATGAATATGATGTCCTAAATCTTAGACACTAC 60
Db 29 ATGGCCAAATTACACGCTGGCACAGAGGATGAATATGATGTCC---TCATAGAGGTGNA 85
Qy 61 CTGGAACAACAGTGGCCCGGACCAAGTT-----CGGGCCCGCGAGTTCTCTCCGCCAG 114
Db 86 CTGGAGAGCGATGAGGCGAGAGCAATGTGACAAGTATGACGCGCCAGGCACTCTCAGCCAG 145
Qy 115 CAGGTGCTGCAAGTTCTGCTGCGCGGTGTTTGGCGGTGCTCTTGGACAACAGTGTCTGGCG 174
Db 146 CTGTGCGCATCAGTCTGCTCTGCTGTTTGTGATCGGTGCTCTGGACAACTCTCTGGTT 205
Qy 175 GTGTTTATCTTTGGTGAATACAAAGGACTCAAGAAATCTGGGGAAACATCTACTTCTTAAC 234
Db 206 GTGCTTATCTCTGGTAAATAATAAAGGACTCAACCGGTGGAAATAATCTATCTTCTTAAC 265
Qy 235 CTGGCACTTTCAAACTGTGTTTCTGCTTCCCTGCGGTCTGGGCCATCTACGACGA 294
Db 266 TTGGCAGTTTCTAACTTGTGTTTCTGCTTACCCTGCGCTTCTGGGCTCATGCTG----- 320
Qy 295 CACGGGAAAGCCCTGCGCAACGGGACCTGTAAGTTCTTGTGGAATCCACTCTCCGGGC 354
Db 321 -----GGGGGATCCCATGTGTGTAATAATTTCTCATTTGACTGTACTTCTGGGC 367
Qy 355 TTATACAGCGAGGTGTTTCCAAACATCTCTCTCTTGTGCAAGGATACAGGGTGTTC 414
Db 368 CTGTACAGTGAAGACATTTTCAATTTGCTTCTGACTGTGCAAGGATACCTAGTGTTC 427
Qy 415 CAAGGGCGAC---TGGGCTTCATCTTCAGCAAGTGTCTTGTGTAATTTGTTGCGTGCATC 471
Db 428 CACAAGGGCAACTTTTCTCAGCCAGGAGGAGGTGCGCTGTGGCATCATTTACAAGTGT 487
Qy 472 CTGGCATGGGCAATGGCTACTGCGCTCTCTTTGCCCGAGTCTGTGTTTATGAGCCTCGG 531
Db 488 CTGGCATGGGTAAAGCCATTTCTGCCACATTTGCTGTAATACGTTGTTTATAAACCTCAG 547
Qy 532 ATGGAAGACAGAAACAAAGTGTGCGCTTTTGGCAAACTCTACTTCTTGGCAATCGAAGCG 591
Db 548 ATGGAAGACAGAAATACAAGTGTGCAATTTAGCAGAACTCTCCTCTGCCAGCTGATGAG 607
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; Publication No. US20030224984A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hans-Peter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scott A.
; APPLICANT: Pan, J.
; APPLICANT: Paoni, N. F.
; APPLICANT: Stephan, J-P F.
; APPLICANT: Watanabe, C.K.
; APPLICANT: Wood, W.I.
; APPLICANT: Williams, P.M.
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: F323SR1C1
; CURRENT APPLICATION NUMBER: US/10/305,654
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homosapiens
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Best Local Similarity 65.58; Pred. No. 3.5e-131;
Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;
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Qy      29 ATGCCCAATTACACGCTGGCCAGCAGGATGATATGATGCC---TCATAGAAGTGAA 85
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Search completed: June 18, 2005, 15:44:37
Job time : 760.748 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 18, 2005, 12:14:55 ; Search time 7463 Seconds
(without alignments)
11024.649 Million cell updates/sec

Title: AF014958
Perfect score: 1698
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Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0
Searched: 4708233 segs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1693.2	99.7	1790	9	AF015525 Homo sapi
3	1675.2	98.7	1755	9	BC071682 Homo sapi
4	1633.4	96.2	1770	9	BC025717 Homo sapi
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6	1468.4	86.5	1475	6	AX490908 Sequence
7	1455.2	85.7	1645	6	CQ882060 Sequence
8	1455.2	85.7	1645	6	AX549068 Sequence
9	1455.2	85.7	143068	6	AX335952 Sequence
10	1455.2	85.7	143068	6	HSU95626 Sequence
11	1453.6	85.6	1645	9	HSU97123 Sequence
12	1452	85.5	1644	6	CQ714577 Sequence
13	1452	85.5	185437	9	AC098613 Homo sapi
14	1449.2	85.3	1546	9	AF015524 Homo sapi
15	1448.2	85.3	1547	6	AR526903 Sequence
16	1268	74.7	1270	6	AR270193 Sequence
17	1033.4	60.9	1035	9	AY337001 Homo sapi
18	1031.8	60.8	1035	6	AX521743 Sequence
19	1028.6	60.6	1035	9	HSA344142 Homo sapi

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	22	950.2	56.0	1035	9	AF124381 Macaca mu
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ALIGNMENTS

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LOCUS Homo sapiens chemokine receptor X (CCRX) mRNA linear PRI 30-OCT-1997
DEFINITION AF014958
ACCESSION AF014958
VERSION AF014958.1 GI:2305263
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1698)
AUTHORS Ansari-Lari, M.A., Liu, X.-M., Gorrell, J.H. and Gibbs, R.A.
TITLE Haplotype analysis of a gene cluster containing CCR5 and a new member of chemokine receptor gene family
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1698)
AUTHORS Ansari-Lari, M.A., Liu, X.-M., Gorrell, J.H. and Gibbs, R.A.
TITLE Direct Submission
JOURNAL Submitted (18-JUL-1997) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
FEATURES
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RESULT 3
LOCUS BC071682 1755 bp mRNA linear PRI 30-JUN-2004
DEFINITION Homo sapiens chemokine (C-C motif) receptor-like 2, mRNA (cdna
clone MGC:87900 IMAGE:5182006), complete cds.

ACCESSION BC071682
VERSION BC071682.1 GI:47939091
KEYWORDS MGC.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 1755)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeb,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,P.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.P., Casavant,T.L.,
Schectt,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,N., Madan,A., Rodriguez,S.,
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Boutard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E.,
Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1755)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (01-JUN-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
COMMENT
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@axil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAP Plate: 166 Row: 1 Column: 1
This clone was selected for full length sequencing because it
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Best Local Similarity 99.8%; Pred. No. 0;
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Db 1 CTGGAGGCTCGGGGAGCTTTTGAGTACTTTTATTTTCAGTTGCTCCCTCAGCTCGGTGAGT 60
QY 79 GGGCGGGTAGAGCCACAGGGGAATCAACAGTGGTTTCTCGTGCCCTCAGGGTCAGA 138
Db 61 GGGCGGGTAGAGCCACAGGGGAATCAACAGTGGTTTCTCGTGCCCTCAGGGTCAGA 120
QY 139 GCAGTCTGATCAAAAGAGGGGATCCACTGTCCGGGGCATTCACACAGCTCCCGGATGC 198
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QY 199 TGGGTCTGAGGCTGCGCCCTTCCCTCGAGGAGCTCAGCCAGTGGGCAGTCTCAAGAT 258
Db 181 TGGGTCTGAGGCTGCGCCCTTCCCTCGAGGAGCTCAGCCAGTGGGCAGTCTCAAGAT 240
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RESULT 4			
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DEFINITION	Homo sapiens chemokine (C-C motif) receptor-like 2, mRNA (cdna clone MGC:34104 IMAGE:5228561), complete cds.		
ACCESSION	BC025717		
VERSION	BC025717.1	GI:19343936	
KEYWORDS	MGC.		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1770)		
	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altshul,S.P., Jordan,B., Buetow,K.H., Schaefer,C.P., Bhat,N.K., Hopkins,R.F., Zordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Donaldson,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raja,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McSwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shvchenko,Y., Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalek,U., Smalus,D.E., Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
AUTHORS	27 (bases 1 to 1770)		
TITLE	Strausberg,R.		
JOURNAL	Direct Submission		
	Submitted (06-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk Email: cgabbs-r@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc_mgc@nih.gov		
	Akhter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,O.L., Mastello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,		

McDowell, J., Pearson, R., Stantripop, S., Thomas, P. J., Touchman, J. W., Tsugeon, C., Vogt, J. L., Walker, M. A., Wetherby, K. D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E. D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 49 Row: 0 Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14043058.

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ORIGIN

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Sequence 15 from Patent WO0208284.
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VERSION
AX454430.1 GI:21713839
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS
Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
TITILE
Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL
Patent: WO 0208284-A 15 31-JAN-2002;
Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone
(US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard,
Audrey (US); Godowski, Paul J. (US); Gurney, Austin L. (US);
Hillan, Kenneth J. (US); Marsters, Scot A. (US); Pan, James (US);
Paoni, Nicholas F. (US); Stephan, Jean-Philippe F. (US);
Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William
I. (US)

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AUTHORS Pettipher,R.
TITLE Receptor proteins
JOURNAL Patent: WO 2004083232-A 1 30-SEP-2004;
Oxagen Limited (GB)
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LOCUS Sequence 353 from Patent WO02061087.
DEFINITION AX549068
ACCESSION AX549068
VERSION AX549068.1 GI:25813844
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Burner,G.C., Roush,C.L. and Brown,J.P.
TITLE Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic peptides

JOURNAL	Patent: WO 02061087-A 353 08-AUG-2002;
LifeSpan Biosciences, Inc. (US)	
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Best Local Similarity	99.8%; Pred. No. 0;
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LOCUS	Sequence 6461 from Patent WO0194629.
DEFINITION	AX335952
ACCESSION	AX335952.1 GI:18126671
VERSION	
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1
AUTHORS	Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE	Cancer gene determination and therapeutic screening using signature gene sets
JOURNAL	Patent: WO 0194629-A 6461 13-DEC-2001;
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CDS	
ORIGIN	Query Match 85.7%; Score 1455.2; DB 9; Length 143068; Best Local Similarity 99.8%; Pred. No. 0; Matches 1457; Conservative 0; Mismatches 3; Indels 0; Gaps 0; QY 239 CCAGTGGGAGTCTGAAGATGCCCAATTACAGCTGGCAGAGATGAATATGATGC 298 DB 96624 CCACAGGGCAGTCTGAAGATGCCCAATTACAGCTGGCAGAGATGAATATGATGC 96683 QY 299 CTCATAGAAGGTGAACACTGAGAGCGCATGAGGCAGAGCAATGTGACAGATATACGCCAC 358 DB 96684 CTCATAGAAGGTGAACACTGAGAGCGCATGAGGCAGAGCAATGTGACAGATATACGCCAC 96743 QY 359 GCACCTCTCAGCCCCAGCTGGTGCCATCATCTGCTCTGCTGTTTGTGATCGGTCCTG 418 DB 96744 GCACCTCTCAGCCCCAGCTGGTGCCATCATCTGCTCTGCTGTTTGTGATCGGTCCTG 96803

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LOCUS
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ACCESSION U97123
VERSION U97123.1 GI:2897070
KEYWORDS
SOURCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1645)
AUTHORS Pan,P., Kyaw,H., Su,K., Zeng,Z., Augustus,M., Carter,K.C. and Li,Y.
TITLE Cloning and characterization of a novel human chemokine receptor
JOURNAL Biochem. Biophys. Res. Commun. 243 (1), 264-268 (1998)
MEDLINE 98139902
PUBMED 9473515
REFERENCE
2 (bases 1 to 1645)
AUTHORS Pan,P., Kyaw,H., Su,K., Shell,B.K., Augustus,M., Carter,K.C. and Li,Y.
TITLE Direct Submission
JOURNAL Submitted (11-APR-1997) Protein Therapeutics, Human Genome
Sciences, Inc., 9410 Key West Ave., Rockville, MD 20850, USA
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RESULT 13

AC098613

LOCUS

DEFINITION

AC098613

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AC098613 185437 bp DNA linear PRI 01-AUG-2002
Homo sapiens chromosome 3 clone RP11-24F11, complete sequence.

AC098613 2 GI:22038607
HTG.

Homo sapiens (human)
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 185437)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.

2 (bases 1 to 185437)
Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.

3 (bases 1 to 185437)
Submitted (26-OCT-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA

4 (bases 1 to 185437)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.

5 (bases 1 to 185437)
Submitted (01-AUG-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA

On Aug 1, 2002 this sequence version replaced gi:16445164.

Center: University of Washington Genome Center
Center Code: UWGC
Web site: <http://www.genome.washington.edu>
Contact: uwgchg@u.washington.edu

Center project name: chr-3
Center clone name: RP11-24F11 (bc0137)
Summary Statistics

Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ET; 93% of reads
Assembly program: Phrap; version 0.990319

Consensus quality: 184860 bases at least Q40
Consensus quality: 185398 bases at least Q30
Consensus quality: 185435 bases at least Q20

Insert size: 185437; sum-of-contigs
Quality coverage: 7.6x in Q20 bases; sum-of-contigs

Overlapping Sequences:
5': BAC-110P12 U95626, 111014-bp overlap
3': RP11-509121 (UWGC:bc0454) AC104304, 61294-bp overlap

Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an
alternate chemistry or covered by high quality data (i.e., Phred
quality >= 30); an attempt was made to resolve all sequencing
problems, such as compressions and repeats; all regions were
covered by at least one plasmid subclone or more than one M13


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VERSION
AF015524.1 GI:3550066
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 1546)
AUTHORS
Gish, K., McClanahan, T. K. and Moore, K. W.
TITLE
CRAM: A Novel Human Chemokine Receptor-Like Gene Expressed in
Activated Monocytes
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 1546)
AUTHORS
Gish, K., McClanahan, T. K. and Moore, K. W.
TITLE
Direct Submission
JOURNAL
Submitted (22-JUL-1997) Molecular Biology, DNAX Research Institute,
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 18, 2005, 12:08:05 ; Search time 957 seconds
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Title: AF014958

Perfect score: 1698

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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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ADP13564

ID ADP13564 standard; DNA; 1698 BP.

XX AC ADP13564;

XX DT 26-AUG-2004 (first entry)

XX DE Renal cell carcinoma differentially expressed gene #300.

XX ds; diagnosis; non-blood disease; solid tumor; gene expression;

KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;

KW head/neck cancer; differential expression.

XX OS Homo sapiens.

XX PN WO2004048933-A2.

XX PD 10-JUN-2004.

XX PF 21-NOV-2003; 2003WO-US037481.

XX PR 21-NOV-2003; 2002US-0427982P.

XX PR 03-APR-2003; 2003US-0459782P.

XX (AMHP) WYETH.

XX (TWIN/) TWINE N C.

XX (BURC/) BURCZYNSKI M E.

XX (TREP/) TREPICCHIO W L.

XX (DORN/) DORNER J A.

XX (STOV/) STOVER J A.

XX (SLON/) SLONI D K.

XX Twine NC, Burczynski ME, Trepicchio WL, Dornier A, Stover JA;

XX Sloni DK;

XX WPI; 2004-460799/43.

XX Diagnosing non-blood disease such as solid tumor, involves comparing differential expression profile of specific genes in peripheral blood sample of subject with reference expression profile of specific genes.

XX Disclosure; SEQ ID NO 300; 350pp; English.

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KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping; gene; ss.
XX Homo sapiens.
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XX WO200200690-A2.
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XX 03-JAN-2002.
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XX 20-JUN-2001; 2001WO-US019692.
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XX 23-JUN-2000; 2000US-0213637P.
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.

PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023322.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
XX (GETH) GENENTECH INC.
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
DR WPI; 2002-090516/12.
XX P-PSDB; ABB84824.
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX Claim 2; Fig 15; 565pp; English.
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC antiangiogenic, hypotensive, vulnery and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The PRO polynucleotides have applications in molecular biology,
CC including use as hybridisation probes, and in chromosome and gene
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC exemplification of the present invention
XX
SQ Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;
Query Match 86.5%; Score 1468.4; DB 6; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 229 GGAGCTCAGCCAGTGGGAGTCTGAGATGCGCAATTTACAGCTGGCCAGAGATGA 288
DB 1 GGAGCTCAGCCAGTGGGAGTCTGAGATGCGCAATTTACAGCTGGCCAGAGATGA 60
QY 289 ATATGATGCTCTCATAGAGGTGAACCTGGAGAGCGATGAGGAGCAATGTGCAAGTA 348

Db 61 ATATGATGTCTCTCATAGAGGGTAACTGGAGAGCGATGAGCGAGCAATGTGACAAGTA 120
Qy 349 TGACGCCAGGCACTCTCAGCCAGCTGGTGCCATCACTCTGTCTCTGCTGTGTTGTGAT 408
Db 121 TGACGCCAGGCACTCTCAGCCAGCTGGTGCCATCACTCTGTCTCTGCTGTGTTGTGAT 180
Qy 409 CGGTGCTCTGGACAAATCTCTGTGTTGTGTTATTCCTGGTAAATATATAAGAGACTCAAACG 468
Db 181 CGGTGCTCTGGACAAATCTCTGTGTTGTGTTATTCCTGGTAAATATATAAGAGACTCAAACG 240
Qy 469 CGTGGAAAAATATCTATCTCTTAACCTGGCAGTTTCTAACTTGCTGTTCTGCTTACCCT 528
Db 241 CGTGGAAAAATATCTATCTCTTAACCTGGCAGTTTCTAACTTGCTGTTCTGCTTACCCT 300
Qy 529 GCCTCTCTGGGCTCATGCTGGGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTT 588
Db 301 GCCTCTCTGGGCTCATGCTGGGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTT 360
Qy 589 CGTGGGCTGTACAGTGAGACATTTTCAATTCGCTTCTGA CTGTGCAAAAGGTACCTAGT 648
Db 361 CGTGGGCTGTACAGTGAGACATTTTCAATTCGCTTCTGA CTGTGCAAAAGGTACCTAGT 420
Qy 649 GTTTTTGCAACAGGCAACTTTTCTCAGCCAGGAGGGTGCCTGTGGCATCATTTAC 708
Db 421 GTTTTTGCAACAGGCAACTTTTCTCAGCCAGGAGGGTGCCTGTGGCATCATTTAC 480
Qy 709 AAGTGTCTGGCATGGTAAACAGCCATTTCTGCGCACCTTTCGCTGAATACGTGGTTTATAA 768
Db 481 AAGTGTCTGGCATGGTAAACAGCCATTTCTGCGCACCTTTCGCTGAATACGTGGTTTATAA 540
Qy 769 ACCTCAGATGGAAGACAGAAATACAAAGTGTGCAATTTAGCAGAACTCCCTTCTGCCAGC 828
Db 541 ACCTCAGATGGAAGACAGAAATACAAAGTGTGCAATTTAGCAGAACTCCCTTCTGCCAGC 600
Qy 829 TGATGAGACATTTCTGAGCAATTTCTGACTTTTAAATTAAGCAATTTGGTCTTGTCCT 888
Db 601 TGATGAGACATTTCTGAGCAATTTCTGACTTTTAAATTAAGCAATTTGGTCTTGTCCT 660
Qy 889 CCCCTATTATTTTACATTTCTCTATGTGCAATGAGAAATGAGAAACACTAAGGTTACAGGA 948
Db 661 CCCCTATTATTTTACATTTCTCTATGTGCAATGAGAAATGAGAAACACTAAGGTTACAGGA 720
Qy 949 GCAGAGGTATAGCCTTTTCAAGCTGTTTTTTCGATAATGGTAGTCTCTCTCTGATGTG 1008
Db 721 GCAGAGGTATAGCCTTTTCAAGCTGTTTTTTCGATAATGGTAGTCTCTCTCTGATGTG 780
Qy 1009 GGGCCCTCAATATTTGCAATTTTCTGTGCTTCTTCAAGAACACTTCTCCTGAGTGA 1068
Db 781 GGGCCCTCAATATTTGCAATTTTCTGTGCTTCTTCAAGAACACTTCTCCTGAGTGA 840
Qy 1069 CTGCAAGAGCAGCTACAATCTGGACAAAGTGTTCACATCACTAAACTCATGCCACCAAC 1128
Db 841 CTGCAAGAGCAGCTACAATCTGGACAAAGTGTTCACATCACTAAACTCATGCCACCAAC 900
Qy 1129 CCACTGCTGCATCAACCCCTCTCTCTGATGCGTTTTCTTGATGGACATTTAGCAAAATACCT 1188
Db 901 CCACTGCTGCATCAACCCCTCTCTCTGATGCGTTTTCTTGATGGACATTTAGCAAAATACCT 960
Qy 1189 CTGCGCCTGTTTCCATCTGGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCA 1248
Db 961 CTGCGCCTGTTTCCATCTGCTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCA 1020
Qy 1249 AGGCACATCGAGGAAGAACCTGACCATTTCCACCGAAGTGTAACTAGCATCCACCAAT 1308
Db 1021 AGGCACATCGAGGAAGAACCTGACCATTTCCACCGAAGTGTAACTAGCATCCACCAAT 1080
Qy 1309 GCAAGAAGATAAACAATGGATTTTTCATCTTTCTGCAATTTTTCATGTAATTTTCTACAC 1368
Db 1081 GCAAGAAGATAAACAATGGATTTTTCATCTTTCTGCAATTTTTCATGTAATTTTCTACAC 1140
Qy 1369 ATTTGTATACAAATCGGATACAGGAAGAAAGGGAGAGGTGAGCTAAACATTTGCTAAGC 1428
Db 1141 ATTTGTATACAAATCGGATACAGGAAGAAAGGGAGAGGTGAGCTAAACATTTGCTAAGC 1200

Qy 1429 ACTGAATTTGTCTCAGGCACCGTGCAAGGCTCTTTTACAAAAGTGAGCTCTTCGCTCCT 1488
Db 1201 ACTGAATTTGTCTCAGGCACCGTGCAAGGCTCTTTTACAAAAGTGAGCTCTTCGCTCCT 1260
Qy 1489 ACCACTTTGTCATAGTGTGGATAGGACTAGTCTCATTTCTCTGAGAAGAAAATAAGGCG 1548
Db 1261 ACCACTTTGTCATAGTGTGGATAGGACTAGTCTCATTTCTCTGAGAAGAAAATAAGGCG 1320
Qy 1549 CGGAATTTGTCTTAGATCACTTAACCTAGGAAGTGCAGAACTGATTTCTCCAGCCCTGGT 1608
Db 1321 CGGAATTTGTCTTAGATCACTTAACCTAGGAAGTGCAGAACTGATTTCTCCAGCCCTGGT 1380
Qy 1609 AGCATTTGCTCAGAGCCTACGCTTGGTCCAGAACATCAAACTCCAAACCTCGGGACAAA 1668
Db 1381 AGCATTTGCTCAGAGCCTACGCTTGGTCCAGAACATCAAACTCCAAACCTCGGGACAAA 1440
Qy 1669 CGACATGAATAAATGATTTTAAACATC 1698
Db 1441 CGACATGAATAAATGATTTTAAACATC 1470

RESULT 4

ABL95568

ID ABL95568 standard; cDNA; 1475 BP.

XX ABL95568;

DT 19-JUL-2002 (first entry)

XX Human angiogenesis related cDNA PRO1873 SEQ ID NO: 15.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
XX atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
XX cardiac; cytostatic; antiangiogenic; hypotensive; vulnerary;
XX antiarteriosclerotic; gene; ss.

OS Homo sapiens.

XX WO200208284-A2.

XX 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US021735.

XX 20-JUL-2000; 2000US-0219556P.

XX 25-JUL-2000; 2000US-0220624P.

XX 25-JUL-2000; 2000US-0220664P.

XX 28-JUL-2000; 2000WO-US020710.

XX 02-AUG-2000; 2000US-0222695P.

XX 17-AUG-2000; 2000US-00643657.

XX 23-AUG-2000; 2000WO-US023522.

XX 24-AUG-2000; 2000WO-US023328.

XX 07-SEP-2000; 2000US-0230978P.

XX 18-SEP-2000; 2000US-00665350.

XX 18-SEP-2000; 2000US-00665350.

XX 24-OCT-2000; 2000US-0242922P.

XX 08-NOV-2000; 2000US-00709258.

XX 08-NOV-2000; 2000WO-US030952.

XX 10-NOV-2000; 2000WO-US030873.

XX 01-DEC-2000; 2000WO-US032678.

XX 20-DEC-2000; 2000US-00747259.

XX 20-DEC-2000; 2000WO-US034956.

XX 22-JAN-2001; 2001US-00767609.

XX 28-FEB-2001; 2001WO-US0096498.

XX 28-FEB-2001; 2001WO-US006520.

XX 01-MAR-2001; 2001WO-US006666.

XX 09-MAR-2001; 2001US-00802706.

XX 14-MAR-2001; 2001US-00808689.

XX 22-MAR-2001; 2001US-00816744.

XX 05-APR-2001; 2001US-00828366.

XX 10-MAY-2001; 2001US-00854208.

XX 10-MAY-2001; 2001US-00854280.

PR	25-MAY-2001;	2001US-00866028.	
PR	25-MAY-2001;	2001US-00866034.	
PR	25-MAY-2001;	2001WO-US017092.	
PR	30-MAY-2001;	2001WO-00870574.	
PR	30-MAY-2001;	2001WO-US017443.	
PR	01-JUN-2001;	2001WO-US017800.	
PR	20-JUN-2001;	2001WO-US019692.	
XX			
PA	(GETH)	GENENTECH INC.	
PA	(BAKE/)	BAKER K P.	
PA	(FERR/)	FERRARA N.	
PA	(GERB/)	GERRITSEN H.	
PA	(GERR/)	GERRITSEN M E.	
PA	(GODD/)	GODDARD A.	
PA	(GODU/)	GODOWSKI P J.	
PA	(GURN/)	GURNEY A L.	
PA	(HILL/)	HILLAN K J.	
PA	(MARS/)	MARSTERS S A.	
PA	(PANJ/)	PAN J.	
PA	(PAONI/)	PAONI N F.	
PA	(STEP/)	STEPHAN J F.	
PA	(WATA/)	WATANABE C K.	
PA	(WILL/)	WILLIAMS P M.	
PA	(WOOD/)	WOOD W I.	
XX			
PI	Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;		
PI	Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;		
PI	Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;		
XX			
DR	WPI; 2002-171999/22.		
DR	P-PSDB; ABB95430.		
XX			
PT	One hundred and eighty seven nucleic acids encoding PRO polypeptides,		
PT	useful in diagnosis and treatment of cardiovascular (e.g. myocardial		
PT	infarction), endothelial or angiogenic disorders in a mammal.		
XX			
PS	Claim 1; Fig 15; 567pp; English.		
XX			
CC	The present invention provides the protein and coding sequences of human		
CC	PRO proteins. These are useful for treating or diagnosing a		
CC	cardiovascular, endothelial or angiogenic disorder, including cardiac		
CC	hypertrophy, trauma, cancer, age-related macular degeneration,		
CC	atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,		
CC	angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumor		
CC	angiogenesis (such as breast carcinoma and liver carcinoma) and wound		
CC	healing. The present sequence is a coding sequence of the invention		
XX			
SQ	Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;		
	Query Match	86.5%;	Score 1468.4; DB 6; Length 1475;
	Best Local Similarity	99.9%;	Pred. No. 0;
	Matches 1469; Conservative	0;	Mismatches 1; Indels 0; Gaps 0;
QY	229	GGAGCTCAGCCAGTGGGCGAGTCTGAAGATGGCCAAATACAGCTGGCCAGCAGAGATGA	288
Db	1	GGAGCTCAGCCAGTGGGCGAGTCTGAAGATGGCCAAATACAGCTGGCCAGCAGAGATGA	50
QY	289	ATATGATGTCTCATAGAAGGTGAATCGAGAGCGGATGAGGAGCAATGTGACAAGTA	348
Db	61	ATATGATGTCTCATAGAAGGTGAATCGAGAGCGGATGAGGAGCAATGTGACAAGTA	120
QY	349	TGACGCCAGGCACTCTCAGCCAGCTGGTGGCATCCTCTGCTGCTGCTTTGTGAT	408
Db	121	TGACGCCAGGCACTCTCAGCCAGCTGGTGGCATCCTCTGCTGCTGCTTTGTGAT	180
QY	409	CGGTGTCTGGCAATCTCTGCTGCTGCTTATCTCTGGTAAATATAAAGGACTCAACG	468
Db	181	CGGTGTCTGGCAATCTCTGCTGCTGCTTATCTCTGGTAAATATAAAGGACTCAACG	240
QY	469	CGTGGAAAATATCTATCTTCTAAACTTGGCAGTTTCTAACTGTGTTTCTGCTTACCT	528
Db	241	CGTGGAAAATATCTATCTTCTAAACTTGGCAGTTTCTAACTGTGTTTCTGCTTACCT	300

QY	529	GCCCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAATAATCTCATTTGGAGCTGACTT	588
Db	301	GCCCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAATAATCTCATTTGGAGCTGACTT	360
QY	589	CGTGGCCCTGTACAGTGTAGACATTTTCAATTTGCCCTTCTGACTGTGTGCAAAAGTACTAGT	648
Db	361	CGTGGCCCTGTACAGTGTAGACATTTTCAATTTGCCCTTCTGACTGTGTGCAAAAGTACTAGT	420
QY	649	GTTTTTGACAAAGGGCAACTTTTCTCAGCCAGGAGGGGTGCCCTGTGGCATCATTTAC	708
Db	421	GTTTTTGACAAAGGGCAACTTTTCTCAGCCAGGAGGGGTGCCCTGTGGCATCATTTAC	480
QY	709	AAGTGTCTGGCATGGGTAAACAGCCATTTCTGGCCACTTTTGCCCTGAATACGTGTTTATAA	768
Db	481	AAGTGTCTGGCATGGGTAAACAGCCATTTCTGGCCACTTTTGCCCTGAATACGTGTTTATAA	540
QY	769	ACCTCAGATGGAAGACCAAGAAATACAAGTGTGCATTTTAGCAGAACTCCCTTCTGCCAGC	828
Db	541	ACCTCAGATGGAAGACCAAGAAATACAAGTGTGCATTTTAGCAGAACTCCCTTCTGCCAGC	600
QY	829	TGATGAGACATCTGGAAAGCAATTTTCTGACTTTTAAATGAACATTTTGGTCTTGTCT	888
Db	601	TGATGAGACATCTGGAAAGCAATTTTCTGACTTTTAAATGAACATTTTGGTCTTGTCT	660
QY	889	CCCCCTATTTTATTTTACATTTCTCTATGTGCAATGAGAAACACATAAGGTTTCAGGA	948
Db	661	CCCCCTATTTTATTTTACATTTCTCTATGTGCAATGAGAAACACATAAGGTTTCAGGA	720
QY	949	GCAGAGGTATAGCCCTTTTCAAGCTTTTGGCCATAATGGTGTGTTCTTCTCTGATGTG	1008
Db	721	GCAGAGGTATAGCCCTTTTCAAGCTTTTGGCCATAATGGTGTGTTCTTCTCTGATGTG	780
QY	1009	GGCGCCCTACATATTGCAATTTTCTGCTGCATTTTCAAGAACACTTCTCCCTCAGTGA	1068
Db	781	GGCGCCCTACATATTGCAATTTTCTGCTGCATTTTCAAGAACACTTCTCCCTCAGTGA	840
QY	1069	CTGCAAGAGCAGCTACAATCTGGACAAAGGTGTTCCATCATCACTAACTCATCGCCACCAC	1128
Db	841	CTGCAAGAGCAGCTACAATCTGGACAAAGGTGTTCCATCATCACTAACTCATCGCCACCAC	900
QY	1129	CCACTGTGTCATCAACCCCTCTCTGTATGCGTTTCTTGATGGGACATTTAGCAATACT	1188
Db	901	CCACTGTGTCATCAACCCCTCTCTGTATGCGTTTCTTGATGGGACATTTAGCAATACT	960
QY	1189	CTGCGCTGTTCATCTGCGTAGTAACACCCACTTCAACCCAGGGGCGAGTCTGCACA	1248
Db	961	CTGCGCTGTTCATCTGCGTAGTAACACCCACTTCAACCCAGGGGCGAGTCTGCACA	1020
QY	1249	AGGCACATCGAGGGAAGAACTCGACCATTTCCACCGAAGTGTAAACTAGCATCCACCAAT	1308
Db	1021	AGGCACATCGAGGGAAGAACTCGACCATTTCCACCGAAGTGTAAACTAGCATCCACCAAT	1080
QY	1309	GCAAGAAGATAAATCATGGAATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1368
Db	1081	GCAAGAAGATAAATCATGGAATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1140
QY	1369	ATTTGTATACAAATTCGATACAGGAAGAAAGGAGAGGTGAGTAACTTGTCTAAGC	1428
Db	1141	ATTTGTATACAAATTCGATACAGGAAGAAAGGAGAGGTGAGTAACTTGTCTAAGC	1200
QY	1429	ACTGAATTTGTCTCAGGCAACCGTCAAGGCTCTTTTACAAACGTGAGCTCTTTCGCTCTCT	1488
Db	1201	ACTGAATTTGTCTCAGGCAACCGTCAAGGCTCTTTTACAAACGTGAGCTCTTTCGCTCTCT	1260
QY	1489	ACCCTTGTCCATAGTGTGGATAGGATCTGCTCAATTTCTGATGTAATAATTTCTACAC	1548
Db	1261	ACCCTTGTCCATAGTGTGGATAGGATCTGCTCAATTTCTGATGTAATAATTTCTACAC	1320
QY	1549	CGGAATTTGTCTAAGATCACTTAATAGGAGTGGCAGAGTGAATCTCCAGCCCTGCT	1608
Db	1321	CGGAATTTGTCTAAGATCACTTAATAGGAGTGGCAGAGTGAATCTCCAGCCCTGCT	1380
QY	1609	AGCATTTGTCTCAGAGCCTACGTTGGTCCAGAACATCAAACTCCAAACCTCCGGGACAAA	1668

Db 1381 AGCAATTTGGCTCAGAGCCTAGCTTGGTCCAGAACATCAAAACCTCGGGACAAA 1440
QY 1669 CGACATGAATAAATGATTTTAAACATC 1698
Db 1441 CGACATGAATAAATGATTTTAAACATC 1470

RESULT 5

ADD10304
ID ADD10304 standard; cDNA; 1475 BP.

XX AC ADD10304;

XX DT 01-JAN-2004 (first entry)

XX DE Human secreted/transmembrane PRO polypeptide cDNA #8.

XX KW ss; gene; human; secreted protein; transmembrane protein; cardiovascular disorder; endothelial disorder; angiogenic disorder; myocardial infarction; cardiac hypertrophy; trauma; cancer;
XX KW age-related macular degeneration; angiogenesis;
XX KW endothelial cell apoptosis; smooth muscle cell growth;
XX KW endothelial cell tube formation.

XX OS Homo sapiens.

XX PN US2003105011-A1.

XX PD 05-JUN-2003.

XX PF 16-AUG-2002; 2002US-00223084.

XX PR 15-SEP-2000; 2000US-0232887P.

XX PR 20-JUN-2001; 2001WO-US019692.

XX PR 09-JUL-2001; 2001WO-US021735.

XX PR 20-FEB-2002; 2002US-00081056.

XX PA (GETH) GENENTECH INC.

XX PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;

XX PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;

XX PI Watanabe CK, Williams PM, Wood WI, Ye W;

XX WPI: 2003-810831/76.

XX P-PSDB; ADD10305.

XX PT New isolated nucleic acid encoding a secreted and transmembrane

XX PT polypeptide for treating a cardiovascular, endothelial, or angiogenic

XX PT disorder in a mammal, such as cancer or age-related macular degeneration.

XX PS Claim 2; SEQ ID NO 15; 493pp; English.

XX CC The invention relates to an isolated nucleic acid encoding a secreted and

XX CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded

XX CC by the nucleic acid, or an agonist or antagonist, is used to treat a

XX CC cardiovascular, endothelial, or angiogenic disorder in a mammal,

XX CC preferably a human. The human may have suffered a myocardial infarction

XX CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular

XX CC degeneration. The cardiac hypertrophy is characterised by the presence of

XX CC an elevated level of PGF-2 alpha. A PRO polypeptide, given in the

XX CC specification, or an agonist is used to inhibit or stimulate endothelial

XX CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac

XX CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.

XX CC PRO302 or an agonist is used to induce endothelial cell apoptosis. A PRO

XX CC polypeptide, given in the specification, or an agonist is used to

XX CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial

XX CC cell tube formation. The present sequence represents a cDNA encoding a

XX CC PRO polypeptide of the invention.

XX SQ Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;

Query Match 86.5%; Score 1468.4; DB 10; Length 1475;

		Best Local Similarity 99.9%; Pzed. No. 0;			
		Matches 1469; Conservative 0; Mismatch 1; Indels 0; Gaps 0;			
QY	229	GGAGCTCAGCCAGTGGGCGAGTCTCAAGATGGCCAAATACAGCTGGCACAGAGATGA	288		
Db	1	GGAGCTCAGCCAGTGGGCGAGTCTCAAGATGGCCAAATACAGCTGGCACAGAGATGA	60		
QY	289	ATATGATGTCTCATAGAAAGGTGAATCGAGAGCCGATGAGGAGAGCAATGTGCAAGTA	348		
Db	61	ATATGATGTCTCATAGAAAGGTGAATCGAGAGCCGATGAGGAGAGCAATGTGCAAGTA	120		
QY	349	TGACGCCAGGCACTCTCAGCCAGCTGGTGCCATCACTCTGCTCTGCTGTGTGTGTAT	408		
Db	121	TGACGCCAGGCACTCTCAGCCAGCTGGTGCCATCACTCTGCTCTGCTGTGTGTGTAT	180		
QY	409	CGGTCTCTGGACAATCTCTGTTGTCTTATCTCTGTTAAATATAAAGGACTCAAAAG	468		
Db	181	CGGTCTCTGGACAATCTCTGTTGTCTTATCTCTGTTAAATATAAAGGACTCAAAAG	240		
QY	469	CCTGGAATAATCTATCTTTCTAAACTTGGCAGTTTCTAACTTGTGTCTTCTTACCCT	528		
Db	241	CCTGGAATAATCTATCTTTCTAAACTTGGCAGTTTCTAACTTGTGTCTTCTTACCCT	300		
QY	529	GCCCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAAATTCATTTGGACTGTACTT	588		
Db	301	GCCCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAAATTCATTTGGACTGTACTT	360		
QY	589	CGTGGGCTGTACAGTGAGACATTTTCAATTTGCCCTCTGACTGTGCAAGGTACTACT	648		
Db	361	CGTGGGCTGTACAGTGAGACATTTTCAATTTGCCCTCTGACTGTGCAAGGTACTACT	420		
QY	649	GTTTTTCACAAAGGCAACTTTTCTCAGCCAGAGAGGGTGCCTCTGTGGCATCATTTAC	708		
Db	421	GTTTTTCACAAAGGCAACTTTTCTCAGCCAGAGAGGGTGCCTCTGTGGCATCATTTAC	480		
QY	709	AAGTGTCTGGCATGGGTAAACAGCCATTTCTGGCCACTTTTGCCTGAATACGTGGTTTATAA	768		
Db	481	AAGTGTCTGGCATGGGTAAACAGCCATTTCTGGCCACTTTTGCCTGAATACGTGGTTTATAA	540		
QY	769	ACCTCAGATGGAGACACCAAGTGCATTTAGCAAGTGCATTTAGCAAGTGCATTTAGCAAG	828		
Db	541	ACCTCAGATGGAGACACCAAGTGCATTTAGCAAGTGCATTTAGCAAGTGCATTTAGCAAG	600		
QY	829	TGATGAGACATTTCTGGAAGCATTTTCTGCACTTTTAAATAATGAACATTTTGGTTCTCT	888		
Db	601	TGATGAGACATTTCTGGAAGCATTTTCTGCACTTTTAAATAATGAACATTTTGGTTCTCT	660		
QY	889	CCCCCTATTTATTTTACATTTCTATGTGCAATGAGAAAAACACATTAAGGTTGAGGA	948		
Db	661	CCCCCTATTTATTTTACATTTCTATGTGCAATGAGAAAAACACATTAAGGTTGAGGA	720		
QY	949	GCAGAGGTATAGCCCTTTTCAAGCTTTTGGCCATATGTTAGTCTTCTTCTCTGATGTG	1008		
Db	721	GCAGAGGTATAGCCCTTTTCAAGCTTTTGGCCATATGTTAGTCTTCTTCTCTGATGTG	780		
QY	1009	GGCGCCCTACAAATTTGCAATTTTCTGCACTTTTCAAGAAACACTTCTCCCTCAGTGA	1068		
Db	781	GGCGCCCTACAAATTTGCAATTTTCTGCACTTTTCAAGAAACACTTCTCCCTCAGTGA	840		
QY	1069	CTGCAAGAGCAGCTACAAATCTGGAACAAAGTGTTCACATCACTAACTCATGCCACCAC	1128		
Db	841	CTGCAAGAGCAGCTACAAATCTGGAACAAAGTGTTCACATCACTAACTCATGCCACCAC	900		
QY	1129	CCACTGTGTCATCAACCTCTCTGTATGCGTTTCTGATGGGACATTTAGCAAAATACCT	1188		
Db	901	CCACTGTGTCATCAACCTCTCTGTATGCGTTTCTGATGGGACATTTAGCAAAATACCT	960		
QY	1189	CTGCGGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGGAGTCTGCACA	1248		
Db	961	CTGCGGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGGAGTCTGCACA	1020		
QY	1249	AGGCACATCGAGGGAAGAACCTGACCAATTCACCGAAGTGTAACTAGCATCCACCAAT	1308		

Db 1021 AGGCATCGAGGGAAGACCTGACCATTCACGAAGTGTAACCTAGCATCCACCAAT 1080
Qy 1309 GCAAGAAGATAAATGATTTTCATCTTTCTGCAATATTTTCATGTAATTTTCTACAC 1368
Db 1081 GCAAGAAGATAAATGATTTTCATCTTTCTGCAATATTTTCATGTAATTTTCTACAC 1140
Qy 1369 ATTTGTATACAAATCGGATACAGGAAGAAAGGAGAGGTGAGCTTAACATTTGCTAAGC 1428
Db 1141 ATTTGTATACAAATCGGATACAGGAAGAAAGGAGAGGTGAGCTTAACATTTGCTAAGC 1200
Qy 1429 ACTGAATTTGTCTCAGGACCGCTGCAAGGCTCTTTTACAAACGTGAGCTCTTCGGCTCT 1488
Db 1201 ACTGAATTTGTCTCAGGACCGCTGCAAGGCTCTTTTACAAACGTGAGCTCTTCGGCTCT 1260
Qy 1489 ACACCTTGTCATAGTGTGGATAGGACTAGTCTCATTTTCTCGAGAAGAAATCTAAGGG 1548
Db 1261 ACCACTTGTCATAGTGTGGATAGGACTAGTCTCATTTTCTCGAGAAGAAATCTAAGGG 1320
Qy 1549 CGGAATTTGTCTAGATCACATTAAGTGAAGAGTGCAGAACTGATTTCTCCAGCCCTGT 1608
Db 1321 CGGAATTTGTCTAGATCACATTAAGTGAAGAGTGCAGAACTGATTTCTCCAGCCCTGT 1380
Qy 1609 AGCATTTGCTCAGAGCTACGCTTGCTCCAGAACATCAAACTCCAAACCTGGGACAAA 1668
Db 1381 AGCATTTGCTCAGAGCTACGCTTGCTCCAGAACATCAAACTCCAAACCTGGGACAAA 1440
Qy 1669 CGACATGAATTAATGTATTTTAAACATC 1698
Db 1441 CGACATGAATTAATGTATTTTAAACATC 1470

RESULT 6

ADD11264
ID ADD11264 standard; cDNA; 1475 BP.
XX
AC ADD11264;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human secreted/transmembrane PRO polypeptide cDNA #8.
XX
KW ss; gene; human; secreted protein; transmembrane protein;
KW cardiovascular disorder; endothelial disorder; angiogenic disorder;
KW myocardial infarction; cardiac hypertrophy; trauma; cancer;
KW age-related macular degeneration; angiogenesis;
KW endothelial cell apoptosis; smooth muscle cell growth;
KW endothelial cell tube formation.
XX
OS Homo sapiens.
XX
PN US2003105013-A1.
XX
PD 05-JUN-2003.
XX
PF 16-AUG-2002; 2002US-00223090.
XX
PR 20-JUN-2001; 2001WO-US019692.
PR 09-JUL-2001; 2001WO-US021735.
PR 20-FEB-2002; 2002US-00081056.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JP;
PI Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2003-801242/75.
DR P-PSDB; ADD11265.
XX
XX
PT New isolated nucleic acid encoding a secreted and transmembrane
PT polypeptide, useful for treating a cardiovascular, endothelial, or
PT angiogenic disorder in a mammal, such as cancer or age-related macular
PT degeneration.

XX Claim 2; SEQ ID NO 15; 493pp; English.
XX
CC The invention relates to an isolated nucleic acid encoding a secreted and
CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
CC by the nucleic acid, or an agonist or antagonist, is used to treat a
CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
CC preferably a human. The human may have suffered a myocardial infarction
CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
CC degeneration. The cardiac hypertrophy is characterised by the presence of
CC an elevated level of pG-2 alpha. A PRO polypeptide, given in the
CC specification, or an agonist is used to inhibit or stimulate endothelial
CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
CC polypeptide, given in the specification, or an agonist is used to
CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
CC cell tube formation. The present sequence represents a cDNA encoding a
CC PRO polypeptide of the invention.
XX
SQ Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;
Query Match 86.5%; Score 1468.4; DB 10; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 229 GGAGCTGAGCCAGTGGGCGAGTCTGAAGATGGCCCAATTACAGCTGGCCACGAGGATGA 288
Db 1 GGAGCTGAGCCAGTGGGCGAGTCTGAAGATGGCCCAATTACAGCTGGCCACGAGGATGA 60
Qy 289 ATATGATGTCCTCATAGAAAGGTGAACCTGGAGAGCGATGAGCGTGGCCACGAGGATGA 348
Db 61 ATATGATGTCCTCATAGAAAGGTGAACCTGGAGAGCGATGAGCGTGGCCACGAGGATGA 120
Qy 349 TGAGCCCGAGGCACTCTCAGCCCGAGCTGGTGCCATCACTCTGCTGCTGTTGTGAT 408
Db 121 TGAGCCCGAGGCACTCTCAGCCCGAGCTGGTGCCATCACTCTGCTGCTGTTGTGAT 180
Qy 409 CGGTGCTCTGACAAATCTCTGGTGTGCTTATCTCTGTAATAATAAAGACTCAAAAG 468
Db 181 CGGTGCTCTGACAAATCTCTGGTGTGCTTATCTCTGTAATAATAAAGACTCAAAAG 240
Qy 469 CGTGAAATATCTATCTTCTAAACTTGGCAGTTTCTAACTTGTGTTTCTTGTACCT 528
Db 241 CGTGAAATATCTATCTTCTAACTTGGCAGTTTCTAACTTGTGTTTCTTGTACCT 300
Qy 529 GCGCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAAATTTCTCATGTGACTACTT 588
Db 301 GCGCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAAATTTCTCATGTGACTACTT 360
Qy 589 CGTGGGCTGTACAGTGAGACATTTTCAATTTGCTTCTGACTGTGCAAGGTACTAGT 648
Db 361 CGTGGGCTGTACAGTGAGACATTTTCAATTTGCTTCTGACTGTGCAAGGTACTAGT 420
Qy 649 GTTTTTCACAAGGCAACTTTTCTCAGCCAGGAGGGTGCCTCTGGCATCATTTAC 708
Db 421 GTTTTTCACAAGGCAACTTTTCTCAGCCAGGAGGGTGCCTCTGGCATCATTTAC 480
Qy 709 AAGTGTCTGGCATGGGTAAACAGCCATTTCTGGCCAATTTTGGCTGAATACGTGGTTATAA 768
Db 481 AAGTGTCTGGCATGGGTAAACAGCCATTTCTGGCCAATTTTGGCTGAATACGTGGTTATAA 540
Qy 769 ACCTCAGATGGAAGCCAGAAATACAGTGTGCAATTTAGCAGAACTCCCTTCTCCAGC 828
Db 541 ACCTCAGATGGAAGCCAGAAATACAGTGTGCAATTTAGCAGAACTCCCTTCTCCAGC 600
Qy 829 TGATGAGACATTTCTGGAAGCATTTTCTGACTTTTAAATTAACATTTTGGTTCTTGTCT 888
Db 601 TGATGAGACATTTCTGGAAGCATTTTCTGACTTTTAAATTAACATTTTGGTTCTTGTCT 660
Qy 889 CCCCTATTTATTTTACATTTCTATGTGCAATATGAGAAAAACATTAAGTTTCAGGA 948
Db 661 CCCCTATTTATTTTACATTTCTATGTGCAATATGAGAAAAACATTAAGTTTCAGGA 720

Qy 949 GCAGAGTATAGCCTTTTCAAGCTGTTGTTTGGCATAATGGTAGCTCTTCTCTCTGATGTG 1008
Db |||||
Qy 721 GCAGAGTATAGCCTTTTCAAGCTGTTGTTTGGCATAATGGTAGCTCTTCTCTGATGTG 780
Db |||||
Qy 1009 GGGCCCTTACAAATATGCAATTTTCCCTGCTCCACTTTCAAGAAACACTTCTCCCTGAGTGA 1068
Db |||||
Qy 781 GGGCCCTTACAAATATGCAATTTTCCCTGCTCCACTTTCAAGAAACACTTCTCCCTGAGTGA 840
Db |||||
Qy 1069 CTGCAAGAGCAGCTACAACTCTGACAAAAGTGTTCACATCACTAAACTCATCGCCACCAC 1128
Db |||||
Qy 841 CTGCAAGAGCAGCTACAACTCTGACAAAAGTGTTCACATCACTAAACTCATCGCCACCAC 900
Db |||||
Qy 1129 CCACTGCTGATCAACCTCTCTCTGATGCGTTTCTTGATGGGACATTTAGCAAAATACCT 1188
Db |||||
Qy 901 CCACTGCTGATCAACCTCTCTCTGATGCGTTTCTTGATGGGACATTTAGCAAAATACCT 960
Db |||||
Qy 1189 CTGCGCTGTTTCCATCTGCTAGTAGTACACCCCACTTCAACCCAGGGGGCAGTCTGCACA 1248
Db |||||
Qy 961 CTGCGCTGTTTCCATCTGCTAGTAGTACACCCCACTTCAACCCAGGGGGCAGTCTGCACA 1020
Db |||||
Qy 1249 AGGCACATCAGGAGGAAGAACTGACCACTTCCACCGAAGTGTAAACTAGCATCCACCAAT 1308
Db |||||
Qy 1021 AGGCACATCAGGAGGAAGAACTGACCACTTCCACCGAAGTGTAAACTAGCATCCACCAAT 1080
Db |||||
Qy 1309 GCAAGAGAAATAACATGGAATTTTCATCTTTCTGCAATTTTTCATGTAATTTTCTACAC 1368
Db |||||
Qy 1081 GCAAGAGAAATAACATGGAATTTTCATCTTTCTGCAATTTTTCATGTAATTTTCTACAC 1140
Db |||||
Qy 1369 ATTGTTATACAAATCGGATACAGGAGAGAAAGAGGAGAGTGAGCTAACTTTGCTAAGC 1428
Db |||||
Qy 1141 ATTGTTATACAAATCGGATACAGGAGAGAAAGAGGAGTGAGCTAACTTTGCTAAGC 1200
Db |||||
Qy 1429 ACTGAAATTTCTCTCAGCACCCTGCAAGGCTCTTTACAACTGAGCTCTCTCGCTCCT 1488
Db |||||
Qy 1201 ACTGAAATTTCTCTCAGCACCCTGCAAGGCTCTTTACAACTGAGCTCTCTCGCTCCT 1260
Db |||||
Qy 1489 ACCACTTTGCTCAGTGTGATAGGACTAGTCTCATTTCTCTGAGAAGAAATAAGGCG 1548
Db |||||
Qy 1261 ACCACTTTGCTCAGTGTGATAGGACTAGTCTCATTTCTCTGAGAAGAAATAAGGCG 1320
Db |||||
Qy 1549 CGGAAATTTGCTTAAGATCACTTAAGTAACTAGGAAAGTGGCAGAACTGTTCTCCAGCCCTGGT 1608
Db |||||
Qy 1321 CGGAAATTTGCTTAAGATCACTTAAGTAACTAGGAAAGTGGCAGAACTGTTCTCCAGCCCTGGT 1380
Db |||||
Qy 1609 AGCAATTTGCTCAGAGCTACGCTTGTGTCAGAGACATCAAACTCCAACTCTGGGGACAA 1668
Db |||||
Qy 1381 AGCAATTTGCTCAGAGCTACGCTTGTGTCAGAGACATCAAACTCCAACTCTGGGGACAA 1440
Db |||||
Qy 1669 CGACATGAAATAAATGTAATTTTAAACATC 1698
Db |||||
Qy 1441 CGACATGAAATAAATGTAATTTTAAACATC 1470
Db |||||

RESULT 7
ADD37057
ID ADD37057 standard; cdna; 1475 BP.
XX
AC ADD37057;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human secreted/transmembrane PRO polypeptide cdna #8.
XX
KW ss; gene; human; secreted protein; transmembrane protein;
KW cardiovascular disorder; endothelial disorder; angiogenic disorder;
KW myocardial infarction; cardiac hypertrophy; trauma; cancer;
KW age-related macular degeneration; angiogenesis;
KW endothelial cell apoptosis; smooth muscle cell growth;
KW endothelial cell tube formation.
XX
OS Homo sapiens.
XX

PN
XX
PD
XX
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PR
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PI
PI
PI
XX
DR
DR
XX
PT
PT
XX
PS
XX
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
SQ
Query Match 86.5%; Score 1468.4; DB 10; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 229 GGAGCTCAGCCAGTGGGCGAGTCTGAAGATGGCCAATTACACGCTGGCAGAGGATGA 288
Db 1 GGAGCTCAGCCAGTGGGCGAGTCTGAAGATGGCCAATTACACGCTGGCAGAGGATGA 60
Qy 289 ATATGATGTCTCATAGAAGTGAATCGAGAGCGATAGGCGAGAGCAATGTGACAAGTA 348
Db 61 ATATGATGTCTCATAGAAGTGAATCGAGAGCGATAGGCGAGAGCAATGTGACAAGTA 120
Qy 349 TCAGCCCGAGGCACTCTCAGCCCGAGTGGTGGCATCACTCTGCTGCTGTTTGTGAT 408
Db 121 TCAGCCCGAGGCACTCTCAGCCCGAGTGGTGGCATCACTCTGCTGCTGTTTGTGAT 180
Qy 409 CGGTGTCTCGGACAAATCTCTGTTGTGCTTATCTCTGGTAAATAATAAAGGACTCAAAACG 468
Db 181 CGGTGTCTCGGACAAATCTCTGTTGTGCTTATCTCTGGTAAATAATAAAGGACTCAAAACG 240
Qy 469 CTTGAAATAATCTATCTTAAACTTGGCAGTTTCTAACTTGTGTTTCTTGTCTTACCCT 528
Db 241 CTTGAAATAATCTATCTTAAACTTGGCAGTTTCTAACTTGTGTTTCTTGTCTTACCCT 300
Qy 529 GCCCTTCTGGGCTCATGCTGGGGGCGATCCCATGTGTAAATAATCTATTGGAGTGTACTT 588
Db 301 GCCCTTCTGGGCTCATGCTGGGGGCGATCCCATGTGTAAATAATCTATTGGAGTGTACTT 360

US2003105012-A1.
05-JUN-2003.
16-AUG-2002; 2002US-00223088.
15-SEP-2000; 2000US-0232887P.
20-JUN-2001; 2001WO-US019692.
09-JUL-2001; 2001WO-US021735.
20-FEB-2002; 2002US-00081056.
(GETH) GENENTECH INC.
Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
Watanabe CK, Williams PM, Wood WI, Ye W;
WPI; 2003-829354/77.
P-PSDB; ADD37058.
New isolated nucleic acids encoding a secreted and transmembrane
polypeptide for treating a cardiovascular, endothelial, or angiogenic
disorder in a mammal, such as cancer or age-related macular degeneration.
Claim 2; SEQ ID NO 15; 492pp; English.

The invention relates to an isolated nucleic acid encoding a secreted and
transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
by the nucleic acid, or an agonist or antagonist, is used to treat a
cardiovascular, endothelial, or angiogenic disorder in a mammal,
preferably a human. The human may have suffered a myocardial infarction
or has cardiac hypertrophy, trauma, a cancer, or age-related macular
degeneration. The cardiac hypertrophy is characterized by the presence of
an elevated level of PGP-2 alpha. A PRO polypeptide, given in the
specification, or an agonist is used to inhibit or stimulate endothelial
cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
polypeptide, given in the specification, or an agonist is used to
stimulate or inhibit smooth muscle cell growth, or to induce endothelial
cell tube formation. The present sequence represents a cdna encoding a
PRO polypeptide of the invention.

Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;

QY 589 CGTGGCCCTGTACGTAGACACATTTTCAATTGCCCTTCTGACTGTGCACAAAGGTACCTAGT 648
DB |||||||
QY 361 CGTGGCCCTGTACGTAGACACATTTTCAATTGCCCTTCTGACTGTGCACAAAGGTACCTAGT 420
DB |||||||
QY 649 GTTTTGTGACAAAGGGCAACTTTTCTCAGCCAGGAGGGTGCCTGTGGCATCATTTAC 708
DB |||||||
QY 421 GTTTTGTGACAAAGGGCAACTTTTCTCAGCCAGGAGGGTGCCTGTGGCATCATTTAC 480
DB |||||||
QY 709 AAGTGTCTGGCATGGTAAAGCCATTTCTGGCCACTTTTGCCTGAATAGTGGTTTATAA 768
DB |||||||
QY 481 AAGTGTCTGGCATGGTAAAGCCATTTCTGGCCACTTTTGCCTGAATAGTGGTTTATAA 540
DB |||||||
QY 769 ACCTCAGATGGAAGCCAGAAATACAAGTGTGCATTTAGCAAACTCCCTCTCCGACG 828
DB |||||||
QY 541 ACCTCAGATGGAAGCCAGAAATACAAGTGTGCATTTAGCAAACTCCCTCTCCGACG 600
DB |||||||
QY 829 TGATGAGACATTTCTGGAACATTTTCTGACTTTTAAATGAACTTTGGTTCTTGTCT 888
DB |||||||
QY 601 TGATGAGACATTTCTGGAACATTTTCTGACTTTTAAATGAACTTTGGTTCTTGTCT 660
DB |||||||
QY 889 CCCCCTATTTTATTTTACATTTCTATGTGCAATGAGAAATGAGAAACACATAAGTTTCAAGGA 948
DB |||||||
QY 661 CCCCCTATTTTATTTTACATTTCTATGTGCAATGAGAAATGAGAAACACATAAGTTTCAAGGA 720
DB |||||||
QY 949 GCAGAGGTATAGCTTTTCAAGCTGTGTTTTCGCATTAATGTTAGTCTTCTCTGATGTG 1008
DB |||||||
QY 721 GCAGAGGTATAGCTTTTCAAGCTGTGTTTTCGCATTAATGTTAGTCTTCTCTGATGTG 780
DB |||||||
QY 1009 GCGCCCTCAATATTTGCAATTTTCTGTCCTTCAAGAAACACTTCTCCCTGAGTGA 1068
DB |||||||
QY 781 GCGCCCTCAATATTTGCAATTTTCTGTCCTTCAAGAAACACTTCTCCCTGAGTGA 840
DB |||||||
QY 1069 CTGCAAGAGCAGTCAATCTCGACAAAGAGTGTTCATCATCTAACTCATGCCACAC 1128
DB |||||||
QY 841 CTGCAAGAGCAGTCAATCTCGACAAAGAGTGTTCATCATCTAACTCATGCCACAC 900
DB |||||||
QY 1129 CCACCTGCTCATCAACCTTCTCTGTATGCTGTTTCTGATGGACATTTAGCAATACCT 1188
DB |||||||
QY 901 CCACCTGCTCATCAACCTTCTCTGTATGCTGTTTCTGATGGACATTTAGCAATACCT 960
DB |||||||
QY 1189 CTGCGCTGTTTCCATCTGCTAGTAAACACCCCACTTCAACCCAGGGGCGAGTCTGCA 1248
DB |||||||
QY 961 CTGCGCTGTTTCCATCTGCTAGTAAACACCCCACTTCAACCCAGGGGCGAGTCTGCA 1020
DB |||||||
QY 1249 AGGCATCTGAGGAAGAACCTGACCAATTCACCGAAGTGTAACTAGCATCCACAAAT 1308
DB |||||||
QY 1021 AGGCATCTGAGGAAGAACCTGACCAATTCACCGAAGTGTAACTAGCATCCACAAAT 1080
DB |||||||
QY 1309 GCAAGAAGATAAACATGATTTTCAATCTTCTGCAATTTTCAATGTAATTTTCTACAC 1368
DB |||||||
QY 1081 GCAAGAAGATAAACATGATTTTCAATCTTCTGCAATTTTCAATGTAATTTTCTACAC 1140
DB |||||||
QY 1369 ATTTGTATACAAATCGGATACAGGAAGAAAGGAGAGGTGAGCTAACTTTGCTAAGC 1428
DB |||||||
QY 1141 ATTTGTATACAAATCGGATACAGGAAGAAAGGAGAGGTGAGCTAACTTTGCTAAGC 1200
DB |||||||
QY 1429 ACTGAATTTGCTCAGGACCGGTGCAAGGCTTTTACAAACGTGAGCTCTTGGCCTCT 1488
DB |||||||
QY 1201 ACTGAATTTGCTCAGGACCGGTGCAAGGCTTTTACAAACGTGAGCTCTTGGCCTCT 1260
DB |||||||
QY 1489 ACCACTGTCCATGTTGATAGGACTAGTCTCATTTCTGAGAGAAACTAAGGCG 1548
DB |||||||
QY 1261 ACCACTGTCCATGTTGATAGGACTAGTCTCATTTCTGAGAGAAACTAAGGCG 1320
DB |||||||
QY 1549 CGGAATTTGCTTAAGATCACTTAACCTAGGAAGTGGCAGAACTGATTTCTCCAGCCCTGT 1608
DB |||||||
QY 1321 CGGAATTTGCTTAAGATCACTTAACCTAGGAAGTGGCAGAACTGATTTCTCCAGCCCTGT 1380
DB |||||||
QY 1609 AGCATTTGCTAGAGCTTACGTTGTTCCAGAACATCAAACTCCAAACCTGCGGACAAA 1668
DB |||||||
QY 1381 AGCATTTGCTAGAGCTTACGTTGTTCCAGAACATCAAACTCCAAACCTGCGGACAAA 1440
DB |||||||
QY 1669 CGCATGAAATAAATGATTTTAAACATC 1698

Db 1441 CGACATGAATAAATGATTTTAAACATC 1470

RESULT 8

ADAE41265
ID ADE41265 standard; cDNA; 1475 BP.

XX ADE41265;

XX 29-JAN-2004 (first entry)

XX Human secreted/transmembrane PRO polypeptide cDNA #8.

XX ss; gene; human; secreted protein; transmembrane protein;
KW cardiovascular disorder; endothelial disorder; angiogenic disorder;
KW myocardial infarction; cardiac hypertrophy; trauma; cancer;
KW age-related macular degeneration; angiogenesis;
KW endothelial cell apoptosis; smooth muscle cell growth;
KW endothelial cell tube formation.

XX Homo sapiens.

XX US2003100497-A1.

XX 29-MAY-2003.

XX 16-AUG-2002; 2002US-00223085.

XX 20-JUN-2001; 2001WO-US019692.

PR 09-JUL-2001; 2001WO-US021735.

PR 20-FEB-2002; 2002US-00081056.

XX (GETH) GENENTECH INC.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;

PI Godowski RJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;

PI Watanabe CK, Williams PM, Wood WI, Ye W;

XX WPI; 2004-008957/01.

DR P-PSDB; ADE41266.

XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO205 or

PT PRO214, useful in molecular biology, chromosome and gene mapping, in

PT generating antisense RNA and DNA, and for treating disorders involving

PT angiogenesis.

XX Claim 2; SEQ ID NO 15; 492pp; English.

XX The invention relates to an isolated nucleic acid encoding a secreted and
CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
CC by the nucleic acid, or an agonist or antagonist, is used to treat a
CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
CC preferably a human. The human may have suffered a myocardial infarction
CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
CC degeneration. The cardiac hypertrophy is characterised by the presence of
CC an elevated level of PGF-2 alpha. A PRO polypeptide, given in the
CC specification, or an agonist is used to inhibit or stimulate endothelial
CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
CC polypeptide, given in the specification, or an agonist is used to
CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
CC cell tube formation. The present sequence represents a cDNA encoding a
CC PRO polypeptide of the invention.

XX Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;

Query Match 86.5%; Score 1468.4; DB 12; Length 1475;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 229 GGAGCTCAGCCCGGCGAGTCTGAAGATGGCCAATTACAGCTGGCACGAGATGA 288

Db 1 GAGCTCAGCCAGTGGCGAGTCTGAAGATGGCCAAATTACACGCTGGCACCAGAGATGA 60
QY 289 ATATGATGTCCTCATAGAGGTGAACCTGGAGAGCGATGAGCGAGAGCAATGTGCAAGTA 348
Db 61 ATATGATGTCCTCATAGAGGTGAACCTGGAGAGCGATGAGCGAGAGCAATGTGCAAGTA 120
QY 349 TGACGCCAGGCACTCTCAGCCCCAGCTGGTGCCATCAGCTCTGCTGTGTGTTGTGAT 408
Db 121 TGACGCCAGGCACTCTCAGCCCCAGCTGGTGCCATCAGCTCTGCTGTGTGTTGTGAT 180
QY 409 CGGTGTCCTGGACAATCTCTGTTGTGTTATCTCTGGTAAATATATAAGGACTCAACG 468
Db 181 CGGTGTCCTGGACAATCTCTGTTGTGTTATCTCTGGTAAATATATAAGGACTCAACG 240
QY 469 CGTGGAAAATATCTATCTCTAACTTGGCAGTTTCTAACTCTGTTTCTGTTTACCCT 528
Db 241 CGTGGAAAATATCTATCTCTAACTTGGCAGTTTCTAACTCTGTTTCTGTTTACCCT 300
QY 529 GCCCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAAATTTCTCAATTGGACTGTACTT 588
Db 301 GCCCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAAATTTCTCAATTGGACTGTACTT 360
QY 589 CGTGGGCTGTACAGTGAGACATTTTCAATTGCCCTTGACTGTGCAAGGTACTAGT 648
Db 361 CGTGGGCTGTACAGTGAGACATTTTCAATTGCCCTTGACTGTGCAAGGTACTAGT 420
QY 649 GTTTTGTGCACAGGGCACTTTTCTCAGCCAGGAGGGTGCCCTGGCATCATTTAC 708
Db 421 GTTTTGTGCACAGGGCACTTTTCTCAGCCAGGAGGGTGCCCTGGCATCATTTAC 480
QY 709 AAGTGTCTGGCATGGTAAACAGCCATCTGCGCCACTTTGCGCTGAATAGTGTGTTTATAA 768
Db 481 AAGTGTCTGGCATGGTAAACAGCCATCTGCGCCACTTTGCGCTGAATAGTGTGTTTATAA 540
QY 769 ACCTCAGATGGAAGACGAGAAATACAAAGTGTGCATTTAGCAGAACTCCTTCTGCGCAGC 828
Db 541 ACCTCAGATGGAAGACGAGAAATACAAAGTGTGCATTTAGCAGAACTCCTTCTGCGCAGC 600
QY 829 TGATGAGACATCTGGAAGCATTTTCTGACTTTTAAATGMACTTTCCGTTCTGTCCT 888
Db 601 TGATGAGACATCTGGAAGCATTTTCTGACTTTTAAATGMACTTTCCGTTCTGTCCT 660
QY 889 CCCCCTATTATTTTACATTTCTATGTGCAATGAGAAACAACTAAGGTTGAGGGA 948
Db 661 CCCCCTATTATTTTACATTTCTATGTGCAATGAGAAACAACTAAGGTTGAGGGA 720
QY 949 GCAGAGGTATAGCCTTTTCAAGCTTTTGGCCATAATGGTAGTCTTCTTCTGATGTG 1008
Db 721 GCAGAGGTATAGCCTTTTCAAGCTTTTGGCCATAATGGTAGTCTTCTTCTGATGTG 780
QY 1009 GGGCGCCTACATATTGCAATTTTCTGTCCTGTCCTTCAAGAACACTTCTCCCTGATGA 1068
Db 781 GGGCGCCTACATATTGCAATTTTCTGTCCTGTCCTTCAAGAACACTTCTCCCTGATGA 840
QY 1069 CTCGAGAGCAGCTACATCTGGACAAAAGTGTTCACATCACTAACTCATGCCACCAC 1128
Db 841 CTCGAGAGCAGCTACATCTGGACAAAAGTGTTCACATCACTAACTCATGCCACCAC 900
QY 1129 CCATGCTGCATCAACCCCTCTCCTGTATGCGTTTCTGTATGGGACATTTAGCAAAATCT 1188
Db 901 CCATGCTGCATCAACCCCTCTCCTGTATGCGTTTCTGTATGGGACATTTAGCAAAATCT 960
QY 1189 CTGCGCCTGTTTCCATCTGCTAGTAAACACCCCATCTTCAAGAACACTTCTCCCTGATGA 1248
Db 961 CTGCGCCTGTTTCCATCTGCTAGTAAACACCCCATCTTCAAGAACACTTCTCCCTGATGA 1020
QY 1249 AGGCACATCGAGGAGAACCTTGACCATTTCCACCGAAGTGAACCTAGCATCCACCAAT 1308
Db 1021 AGGCACATCGAGGAGAACCTTGACCATTTCCACCGAAGTGAACCTAGCATCCACCAAT 1080
QY 1309 GCAAGAAGAAATAACATGGATTTTTCATCTTCTGCAATTTTTCATGTAATTTTCTACAC 1368

Db 1081 GCAAGAAGAAATAACATGGATTTTTCATCTTCTGCAATTTTTCATGTAATTTTCTACAC 1140
QY 1369 ATTTGTATACAAATCGGATACAGGAAGAAAGGGAGAGGTAGCTAAACATTTTCTAAGC 1428
Db 1141 ATTTGTATACAAATCGGATACAGGAAGAAAGGGAGAGGTAGCTAAACATTTTCTAAGC 1200
QY 1429 ACTGAATTTGTCTCAGGCAACCGTGCAAGGCTCTTTTACAAACGTGAGCTCTTCTGCGCTCT 1488
Db 1201 ACTGAATTTGTCTCAGGCAACCGTGCAAGGCTCTTTTACAAACGTGAGCTCTTCTGCGCTCT 1260
QY 1489 ACCACTTGTCCATAGTGTGGATAGGACTAGTCTCATTTCTCTGAGAAGAAACTAAGGCG 1548
Db 1261 ACCACTTGTCCATAGTGTGGATAGGACTAGTCTCATTTCTCTGAGAAGAAACTAAGGCG 1320
QY 1549 CGGAATTTGTCTAAGATCACTTAACTAGGAAGTGCAGAACTGATTTCCAGCCCTGGT 1608
Db 1321 CGGAATTTGTCTAAGATCACTTAACTAGGAAGTGCAGAACTGATTTCCAGCCCTGGT 1380
QY 1609 AGCATTTGTCTCAGAGCTACGCTTGGTCCAGAACATCAAACTCCAAACCTTGGGACAAA 1668
Db 1381 AGCATTTGTCTCAGAGCTACGCTTGGTCCAGAACATCAAACTCCAAACCTTGGGACAAA 1440
QY 1669 CGACATGAAATAAATGATTTTAAACATC 1698
Db 1441 CGACATGAAATAAATGATTTTAAACATC 1470

RESULT 9
ADH43448
ID ADH43448 standard; cDNA; 1475 BP.
XX
AC ADH43448;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human PRO polynucleotide #8.
XX
KW Human; PRO; gene; ss; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; endothelial cell growth; cardiac hypertrophy;
KW cell apoptosis; cell tube formation; angiogenesis;
KW smooth muscle cell growth; myocardial infarction; trauma; cancer;
KW age-related macular degeneration; cytostatic; cardiant;
KW cerebroprotective; ophthalmological; vulnerary.
XX
OS Homo sapiens.
XX
PN US2003224984-A1.
XX
PD 04-DEC-2003.
XX
PF 26-NOV-2002; 2002US-00305654.
XX
PR 20-JUN-2001; 2001WO-US019692.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritson ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pen J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WL, Ye W;
XX
DR WPI; 2004-042166/04.
XX
DR P-PSDB; ADH43449.
XX
PT New PRO polypeptides and nucleic acids encoding the polypeptides, useful
PT for treating myocardial infarction, cardiac hypertrophy, trauma, cancer,
PT or age-related macular degeneration.
XX
PS Claim 2; SEQ ID NO 15; 492pp; English.
XX
CC The invention relates to human PRO polypeptides and the PRO
CC polynucleotides encoding them. The invention also relates to treating
CC cardiovascular, endothelial or angiogenic disorders in mammals,
CC inhibiting endothelial cell growth, stimulating endothelial cell growth,

CC inducing cardiac hypertrophy, cell apoptosis or cell tube formation and
 CC stimulating angiogenesis or smooth muscle cell growth by administering
 CC polypeptides of the invention. The PRO polypeptides and polynucleotides
 CC are useful for treating cardiovascular, endothelial or angiogenic
 CC disorders, e.g. myocardial infarction, cardiac hypertrophy, trauma,
 CC cancer or age-related macular degeneration. The PRO polynucleotides are
 CC useful as hybridisation probes in chromosome and gene mapping and in
 CC generating antisense RNA and DNA, and for chromosome identification and
 CC tissue typing. The PRO polypeptides and polynucleotides are also useful
 CC in gene therapy and as molecular weight markers for protein
 CC electrophoresis purposes. This sequence represents a human PRO
 CC polynucleotide of the invention.

XX
 SQ Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;

Query Match 86.5%; Score 1468.4; DB 12; Length 1475;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	229	GGAGCTCAGCCAGTGGGAGTCTGAGATGCGCAATACAGCTGGCCACGAGATGA	288
DB	1	GGAGCTCAGCCAGTGGGAGTCTGAGATGCGCAATACAGCTGGCCACGAGATGA	60
QY	289	ATATGATGTCTCATAGAGGTGAATCGAGAGCGATGAGGAGCAATGTGACAAGTA	348
DB	61	ATATGATGTCTCATAGAGGTGAATCGAGAGCGATGAGGAGCAATGTGACAAGTA	120
QY	349	TGAGCCGAGGCACTCTCAGCCAGCTGTGCGATCACTCTCTCTGTGTGTGTGTAT	408
DB	121	TGAGCCGAGGCACTCTCAGCCAGCTGTGCGATCACTCTCTCTGTGTGTGTGTAT	180
QY	409	CGGTGTCTGGCAATCTCTGGTGTGCTTATCTGCTTAAATATTAAGGACTCAACG	468
DB	181	CGGTGTCTGGCAATCTCTGGTGTGCTTATCTGCTTAAATATTAAGGACTCAACG	240
QY	469	CGTGGAAATATCTATCTTAAACTTGGCAGTTTCTAACTTGTGTCTTCTTACCT	528
DB	241	CGTGGAAATATCTATCTTAAACTTGGCAGTTTCTAACTTGTGTCTTCTTACCT	300
QY	529	GCCCTTCTGGCTCATGTCTGGGGGATCCCATGTGTAATTCATTTGGACTGTACTT	588
DB	301	GCCCTTCTGGCTCATGTCTGGGGGATCCCATGTGTAATTCATTTGGACTGTACTT	360
QY	589	CGTGGGCTGACGTGAGACATTTTCAATTTGCTTCTGACGTGCAAGGTACTAGT	648
DB	361	CGTGGGCTGACGTGAGACATTTTCAATTTGCTTCTGACGTGCAAGGTACTAGT	420
QY	649	GTTTTGTGCAAGGGGCAACTTTTCTCAGCCAGGAGGGTGCCTCTGGCATCATTTAC	708
DB	421	GTTTTGTGCAAGGGGCAACTTTTCTCAGCCAGGAGGGTGCCTCTGGCATCATTTAC	480
QY	709	AAAGTGTCTGGCATGGTTAAAGCCATTTCTGCGCACTTTTGCCTGAATAGTGGTTATAA	768
DB	481	AAAGTGTCTGGCATGGTTAAAGCCATTTCTGCGCACTTTTGCCTGAATAGTGGTTATAA	540
QY	769	ACCTCAGATGGAGCCAGAAATACAGTGTGCATTTAGCAACTCCCTTCTGCCAGC	828
DB	541	ACCTCAGATGGAGCCAGAAATACAGTGTGCATTTAGCAACTCCCTTCTGCCAGC	600
QY	829	TGATGAGACATTTCTGGAAGCATTTTCTGACTTTTAAATGAAATTCGTTTGTGCT	888
DB	601	TGATGAGACATTTCTGGAAGCATTTTCTGACTTTTAAATGAAATTCGTTTGTGCT	560
QY	889	CCCCCTATTTTATTTTACATTTCTCTATGTGCAATGAGAAACACATAAGTTTCAGGA	948
DB	661	CCCCCTATTTTATTTTACATTTCTCTATGTGCAATGAGAAACACATAAGTTTCAGGA	720
QY	949	CGAGAGGTATAGCTTTTCAAGCTGTTTTCGCTATAGGTAGTCTTCTCTCTGATGTG	1008
DB	721	CGAGAGGTATAGCTTTTCAAGCTGTTTTCGCTATAGGTAGTCTTCTCTCTGATGTG	780
QY	1009	GGCGCCCTACAATATTTGCAATTTTCTCTGTCACATTTTCAAGAACACTTCTCCCTGAGTGA	1068

DB	781	GGGCGCCTACAATATTGCAATTTTCTCTGTCACATTTTCAAAGAACACTTCTCCCTGAGTGA	840
QY	1069	CTGCAAGAGCAGCTACAATCTGGACAAAGTGTTCACATCACTAACTCATCGCCACCAC	1128
DB	841	CTGCAAGAGCAGCTACAATCTGGACAAAGTGTTCACATCACTAACTCATCGCCACCAC	900
QY	1129	CCACTGCTGCATCAACCCCTCTCTGTATGCGTTTCTTGATGGGACATTTAGCAATATACCT	1188
DB	901	CCACTGCTGCATCAACCCCTCTCTGTATGCGTTTCTTGATGGGACATTTAGCAATATACCT	960
QY	1189	CTGCGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACA	1248
DB	961	CTGCGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACA	1020
QY	1249	AGGCACATCGAGGGAAGAACCTCGACCATTCACCCGAGGTGTAACCTAGCATCCACAAT	1308
DB	1021	AGGCACATCGAGGGAAGAACCTCGACCATTCACCCGAGGTGTAACCTAGCATCCACAAT	1080
QY	1309	GCAAGAACATAAATACATGATTTTTCATCTTCTGCAATTTTTCATGTAATTTTCTACAC	1368
DB	1081	GCAAGAACATAAATACATGATTTTTCATCTTCTGCAATTTTTCATGTAATTTTCTACAC	1140
QY	1369	ATTGTATATAAAATTCGGATACAGGAAGGAGGAGGTGAGCTAATTTTGTAAAGC	1428
DB	1141	ATTGTATATAAAATTCGGATACAGGAAGGAGGAGGTGAGCTAATTTTGTAAAGC	1200
QY	1429	ACTGAATTTGCTCAGGCAACGCTGCAAGGCTTTTACAAACGTGAGCTCTTCCGCTCCT	1488
DB	1201	ACTGAATTTGCTCAGGCAACGCTGCAAGGCTTTTACAAACGTGAGCTCTTCCGCTCCT	1260
QY	1489	ACCCTTCTGCATAGTGTGGATAGGACTAGTCTCAATTTCTTGAGAGAAACTAAGGCG	1548
DB	1261	ACCCTTCTGCATAGTGTGGATAGGACTAGTCTCAATTTCTTGAGAGAAACTAAGGCG	1320
QY	1549	CGGAAATTTGCTTAAGATCACTTAACCTAGGAGTGGGAGAACTGATTTCTCCAGCCCTGGT	1608
DB	1321	CGGAAATTTGCTTAAGATCACTTAACCTAGGAGTGGGAGAACTGATTTCTCCAGCCCTGGT	1380
QY	1609	AGCATTTGCTCAGAGCCTACGCTTGGTCCAGAACATCAAACTCCAAACCTGGGGACAAA	1668
DB	1381	AGCATTTGCTCAGAGCCTACGCTTGGTCCAGAACATCAAACTCCAAACCTGGGGACAAA	1440
QY	1669	CGACATGAAATAAATGATTTTAAACATC	1698
DB	1441	CGACATGAAATAAATGATTTTAAACATC	1470

RESULT 10

ADK82793

ID ADK82793 standard; cDNA; 1475 BP.

XX ADK82793;

XX 20-MAY-2004 (first entry)

XX Human PRO polynucleotide #8.

XX Human; PRO; gene; 86; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; endothelial cell growth; cardiac hypertrophy;
 KW cell apoptosis; cell tube formation; angiogenesis;
 KW smooth muscle cell growth; myocardial infarction; trauma; cancer;
 KW age-related macular degeneration; cytoskeletal; cardiant;
 KW cerebroprotective; ophthalmological; vulnary.

OS Homo sapiens.

XX US2004043927-A1.

XX 04-MAR-2004.

XX 20-FEB-2002; 2002US-00081056.

XX 19-SEP-1997; 97US-00933821.

PR 29-JAN-1998; 98US-00015089.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 15-NOV-1998; 98US-0180997.
PR 01-DEC-1998; 98WO-US025108.
PR 23-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99WO-US000106.
PR 12-FEB-1999; 99US-00214186.
PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99WO-US005028.
PR 03-MAR-1999; 99US-00254460.
PR 12-MAR-1999; 99US-00267213.
PR 12-APR-1999; 99US-00284291.
PR 02-JUN-1999; 99WO-US013252.
PR 14-JUN-1999; 99US-00332928.
PR 14-JUN-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 15-OCT-1999; 99US-00403154.
PR 18-OCT-1999; 99US-00403296.
PR 18-OCT-1999; 99US-00403297.
PR 10-NOV-1999; 99US-00423741.
PR 12-NOV-1999; 99US-00423843.
PR 12-NOV-1999; 99US-00423844.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 16-DEC-1999; 99WO-US030099.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006684.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 05-APR-2001; 2001US-00828366.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 13-AUG-2001; 2001US-00929404.
PR 16-AUG-2001; 2001US-00931836.
PR 28-AUG-2001; 2001US-00941992.
PR 04-SEP-2001; 2001US-00946374.
PR 07-SEP-2001; 2001US-00948901.
PR 15-NOV-2001; 2001US-00002796.
PR 30-NOV-2001; 2001US-00001054.
PR 06-DEC-2001; 2001US-00006867.
PR 19-DEC-2001; 2001US-00028072.
PR 15-JAN-2002; 2002US-00052586.
PR 17-JAN-2002; 2002US-00053107.
PR 18-JAN-2002; 2002US-00052594.
PR 08-FEB-2002; 2002US-00072068.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JP;
PI Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI; 2004-225727/21.
DR P-PSDB; ADK82794.
XX
PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
PS Claim 2; SEQ ID NO 15; 494pp; English.
XX
CC The invention relates to human PRO polypeptides and the PRO
CC polynucleotides encoding them. The invention also relates to treating
CC cardiovascular, endothelial or angiogenic disorders in mammals,
CC inhibiting endothelial cell growth, stimulating endothelial cell growth,
CC inducing cardiac hypertrophy, cell apoptosis or cell tube formation and
CC stimulating angiogenesis or smooth muscle cell growth by administering
CC polypeptides of the invention. The PRO polypeptides and polynucleotides
CC are useful for treating cardiovascular, endothelial or angiogenic
CC disorders, e.g. myocardial infarction, cardiac hypertrophy, trauma,
CC cancer or age-related macular degeneration. The PRO polynucleotides are
CC useful as hybridisation probes in chromosome and gene mapping and in
CC generating antisense RNA and DNA, and for chromosome identification and
CC tissue typing. The PRO polypeptides and polynucleotides are also useful
CC in gene therapy and as molecular weight markers for protein
CC electrophoresis purposes. This sequence represents a human PRO
CC polynucleotide of the invention. Note: The sequence data for this patent
CC is also available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;
Query Match 86.5%; Score 1468.4; DB 12; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 229 GGAGCTCAGCCCGTGGGCGAGTCTGAAGATGGCCCAATTACACGCTGGCACCAGAGATGA 288

1 GAGAGCTCAGCCAGTGGGCGAGTCTGAAATGGCCAAATTAACGCTGGCCACGAGATGA 60
289 ATATGATGTCCTCATAGAAGGTGAATCGGAGAGCGGATGAGGAGCAAGTGTGACAAGTA 348
61 ATATGATGTCCTCATAGAAGGTGAATCGGAGAGCGGATGAGGAGCAAGTGTGACAAGTA 120
349 TGAAGCCAGGCACTCTCAGCCAGCTGGTGCCATCACTCTGCTCTGCTGTGTTGTGAT 408
121 TGAAGCCAGGCACTCTCAGCCAGCTGGTGCCATCACTCTGCTCTGCTGTGTTGTGAT 180
409 CGGTGTCCTGGCAATCTCTGCTGTGCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 468
181 CGGTGTCCTGGCAATCTCTGCTGTGCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
469 CGTGGAAAATATCTATCTTCTTAACTTGGCAGTTCTAACTGTGTTCTTCTGCTTACCT 528
241 CGTGGAAAATATCTATCTTCTTAACTTGGCAGTTCTAACTGTGTTCTTCTGCTTACCT 300
529 GCCCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAATAATCTCATTTGGACTGTACTT 588
301 GCCCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAATAATCTCATTTGGACTGTACTT 360
589 CGTGGGCTGTACAGTGAGACATTTTTCAATTTGCCCTTCTGACTGTGCAAGAGTACTAGT 648
361 CGTGGGCTGTACAGTGAGACATTTTTCAATTTGCCCTTCTGACTGTGCAAGAGTACTAGT 420
649 GTTTTGGCAAGGGCAACTTTTTCTCAGCCAGGAGGGTGCCCTCTCGGCATCATTTAC 708
421 GTTTTGGCAAGGGCAACTTTTTCTCAGCCAGGAGGGTGCCCTCTCGGCATCATTTAC 480
709 AGTGTCTGGGATGGGTAAAGCCATTTCTGGCCACTTTGCTGTAATAGTGGTTTAA 768
481 AGTGTCTGGGATGGGTAAAGCCATTTCTGGCCACTTTGCTGTAATAGTGGTTTAA 540
769 ACTCAGATGGAAGCAGCAATATCAAGTGTGCATTTAGCAGAACTCCCTCTCGCCAGC 828
541 ACTCAGATGGAAGCAGCAATATCAAGTGTGCATTTAGCAGAACTCCCTCTCGCCAGC 600
829 TGATGAGACATTTCTGGAAGCATTTTCTGACTTTAAATAATGAACATTTGGTTCTGTCT 888
601 TGATGAGACATTTCTGGAAGCATTTTCTGACTTTAAATAATGAACATTTGGTTCTGTCT 660
889 CCCCTATTATTTTACATTTCTATGTGCAATGAGAAAACACTAAGTTTCAGGA 948
661 CCCCTATTATTTTACATTTCTATGTGCAATGAGAAAACACTAAGTTTCAGGA 720
949 GCAGAGGTATAGCCTTTTCAAGCTTGTGTTTGGCCATATGTTGCTCTCTCTGATGTG 1008
721 GCAGAGGTATAGCCTTTTCAAGCTTGTGTTTGGCCATATGTTGCTCTCTCTGATGTG 780
1009 GGGGCGCCTACAATATGTCATTTTCTGTGCTCACTTTCAAGAACACTTCTCCCTGAGTGA 1068
781 GGGGCGCCTACAATATGTCATTTTCTGTGCTCACTTTCAAGAACACTTCTCCCTGAGTGA 840
1069 CTGCAAGAGCAGTCAATCTCGACAAAAGTGTTCACATCACTAACTCATCGCCACCAC 1128
841 CTGCAAGAGCAGTCAATCTCGACAAAAGTGTTCACATCACTAACTCATCGCCACCAC 900
1129 CCATGCTGCTCATCAACCCCTCTCTGTATGCGTTTCTTGATGGACATTTAGCAAAATACCT 1188
901 CCATGCTGCTCATCAACCCCTCTCTGTATGCGTTTCTTGATGGACATTTAGCAAAATACCT 960
1189 CTCGCGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACA 1248
961 CTCGCGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACA 1020
1249 AGGCATCTGAGGAGAACCTTGACCATTCACCGAGTGAATAGCATCCCAAT 1308
1021 AGGCATCTGAGGAGAACCTTGACCATTCACCGAGTGAATAGCATCCCAAT 1080
1309 GCAAGAAGATAAATCATGATTTTCTATCTTCTGCTGATTTTCTATGTAATTTCTACAC 1368

1081 GCAGAGAATAAATCAATGATTTTTCATCTTCTGCTGATTTTTCATGTAATTTTCTACAC 1140
1369 ATTTCTATACAAAATCGGATACAGAAAGAAAGGAGAGGTGAGCTAAATTTTGTAAAGC 1428
1141 ATTTCTATACAAAATCGGATACAGAAAGAAAGGAGAGGTGAGCTAAATTTTGTAAAGC 1200
1429 ACTGAATTTGCTCAGGCACCGTGAAGGCTTTTCAAAAGTGAAGTCTTCTGCGCTCCT 1488
1201 ACTGAATTTGCTCAGGCACCGTGAAGGCTTTTCAAAAGTGAAGTCTTCTGCGCTCCT 1260
1489 ACCACTTCTCATAGTGTGGATAGGACTAGTCTCATTTTCTCTGAGAAGAAAACCTAAGGCG 1548
1261 ACCACTTCTCATAGTGTGGATAGGACTAGTCTCATTTTCTCTGAGAAGAAAACCTAAGGCG 1320
1549 CGGAAATTTGCTTAAGATCACCTTAAGAGGAGTGGAGAACTGATTTCTCCAGCCCTGCT 1608
1321 CGGAAATTTGCTTAAGATCACCTTAAGAGGAGTGGAGAACTGATTTCTCCAGCCCTGCT 1380
1609 AGCATTTTCTCAGAGCCCTACGCTTGGTCCAGAACATCAAACTCCAAACCTCGGGACAAA 1668
1381 AGCATTTTCTCAGAGCCCTACGCTTGGTCCAGAACATCAAACTCCAAACCTCGGGACAAA 1440
1669 CGACATGAAATAAATGATTTTAAACATC 1698
1441 CGACATGAAATAAATGATTTTAAACATC 1470

RESULT 11
ABZ42782

ID ABZ42782 standard; DNA; 1645 BP.

XX ABZ42782;

XX 04-MAR-2003 (first entry)

XX Human chemokine receptor-like 2 nucleotide SEQ ID NO:353.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
XX G protein-coupled receptor modulator; antibody; immune-related disease;
XX growth-related disease; cell regeneration-related disease; AIDS; cancer;
XX immunological-related cell proliferative disease; autoimmune disease;
XX Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
XX osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
XX graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
XX psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
XX mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
XX hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
XX ulcer; gene; ds.

XX Homo sapiens.

XX WO200261087-A2.

XX 08-AUG-2002.

XX 19-DEC-2001; 2001WO-US050107.

XX 19-DEC-2000; 2000US-0257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burner GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

XX P-PSDB; ABP81934.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors
XX (GPCR), useful for diagnosing and designing drugs for treating conditions
XX in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
XX autoimmune diseases.

XX Disclosure; Fig 1; 523pp; English.

CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 1645 BP; 443 A; 383 C; 361 G; 458 T; 0 U; 0 Other;

Query Match 85.7%; Score 1455.2; DB 8; Length 1645;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1457; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 239 CCAGTGGGAGTCTGAAGATGGCCAAATTACGCTGGCACCAGAGGATGAATGATGTC 298
DB 185 CCACAGGGCAGTCTGAAGATGGCCAAATTACGCTGGCACCAGAGGATGAATGATGTC 244
QY 299 CTCATAGAAGTGAAGTGGAGAGCGATGAGGAGAGCAATGTGCAAGTATGACGCCAG 358
DB 245 CTCATAGAAGTGAAGTGGAGAGCGATGAGGAGAGCAATGTGCAAGTATGACGCCAG 304
QY 359 GCATCTCAGCCAGCTGGTGCATCACTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 418
DB 305 GCATCTCAGCCAGCTGGTGCATCACTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 364
QY 419 GACAATCTCTGGT 478
DB 365 GACAATCTCTGGT 424
QY 479 ATCTATCTTTCTAACTTGGCAGTTTCTAACTTGTGTGTGTGTGTGTGTGTGTGTGTGT 538
DB 425 ATCTATCTTTCTAACTTGGCAGTTTCTAACTTGTGTGTGTGTGTGTGTGTGTGTGTGT 484
QY 539 GCTCATGCTGGGGCGATCCCATGTGTAAATTTCTATTTGAGTGTACTTGTGGGCGCTG 598
DB 485 GCTCATGCTGGGGCGATCCCATGTGTAAATTTCTATTTGAGTGTACTTGTGGGCGCTG 544
QY 599 TACAGTGAGACATTTTCTCAATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 658
DB 545 TACAGTGAGACATTTTCTCAATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 604
QY 659 AAGGGCAACTTTTCTCAGCCAGGAGGAGGTCCTGTGGCATCAATTACAAAGTGTCTGTG 718
DB 605 AAGGGCAACTTTTCTCAGCCAGGAGGAGGTCCTGTGGCATCAATTACAAAGTGTCTGTG 664
QY 719 GCATGGGTAAAGCCATTTCTGGCCATTTGGTGTGAATACGTGGTTTATAAACCTCAGATG 778
DB 665 GCATGGGTAAAGCCATTTCTGGCCATTTGGTGTGAATACGTGGTTTATAAACCTCAGATG 724
QY 779 GAAGACCAAGATACAAAGTGTGATTTAGCAGAACTCCCTTCTGTCAGCTGATGAGACA 838
DB 725 GAAGACCAAGATACAAAGTGTGATTTAGCAGAACTCCCTTCTGTCAGCTGATGAGACA 784
QY 839 TTCTGGAAGCATTTTCTGACTTTTAAATAATGAACATTTTCGTTCTTCTGTCCTCCCTATT 898

DB 785 TTCTGGAAGCATTTTCTGACTTTTAAATAATGAACATTTTCGTTCTTCTGTCCTCCCTATT 844
QY 899 ATTTTACATTTCTCTATGTGCATAATGAGAAAACACTAAGGTTTCAGGGAGCAGAGTAT 958
DB 845 ATTTTACATTTCTCTATGTGCATAATGAGAAAACACTAAGGTTTCAGGGAGCAGAGTAT 904
QY 959 AGCTTTTCAAGCTGTGTTTTGTCATAATAGTGTCTTCTCTGTGATGTGGGCGCCCTAC 1018
DB 905 AGCTTTTCAAGCTGTGTTTTGTCATAATAGTGTCTTCTCTGTGATGTGGGCGCCCTAC 964
QY 1019 AATATTGCATTTTCTGTCCTCACTTTTCAAGAAACACTTCTCTCTGTGATGTGCAAGAGC 1078
DB 965 AATATTGCATTTTCTGTCCTCACTTTTCAAGAAACACTTCTCTCTGTGATGTGCAAGAGC 1024
QY 1079 AGCTACAATCTGCAGAAAAGTGTTCACATCACTTAAACTCATTCGCCACCCCACTGCTGC 1138
DB 1025 AGCTACAATCTGCAGAAAAGTGTTCACATCACTTAAACTCATTCGCCACCCCACTGCTGC 1084
QY 1139 ATCAACCCCTCTCTGTATGCGTTTCTGTATGGGACATTTAGCAAAATACCTCTGCGCGTGT 1198
DB 1085 ATCAACCCCTCTCTGTATGCGTTTCTGTATGGGACATTTAGCAAAATACCTCTGCGCGTGT 1144
QY 1199 TTCCATCTCGGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACAAGGCACATCG 1258
DB 1145 TTCCATCTCGGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACAAGGCACATCG 1204
QY 1259 AGGGAAGACCTGACCNTTCCACCCGAAAGTGTAAACTAGCATCCACCAATGCAAGAGAA 1318
DB 1205 AGGGAAGACCTGACCNTTCCACCCGAAAGTGTAAACTAGCATCCACCAATGCAAGAGAA 1264
QY 1319 TAAACATGATTTTCTGCAATTTTCTGCAATTTTCTGCAATTTTCTGCAATTTTCTGCAAT 1378
DB 1265 TAAACATGATTTTCTGCAATTTTCTGCAATTTTCTGCAATTTTCTGCAATTTTCTGCAAT 1324
QY 1379 AAAATCGGATACAGGAAGAAAAGGGAGAGGTGAGCTTAAACATTTTCTGCAATTTTCTGCAAT 1438
DB 1325 AAAATCGGATACAGGAAGAAAAGGGAGAGGTGAGCTTAAACATTTTCTGCAATTTTCTGCAAT 1384
QY 1439 TCTCAGGACCCGTGCAAGCTCTTTTACAAACGTGAGCTCTTCTGCGCTCTTACCACTTGTG 1498
DB 1385 TCTCAGGACCCGTGCAAGCTCTTTTACAAACGTGAGCTCTTCTGCGCTCTTACCACTTGTG 1444
QY 1499 CATAGTGTGATAGTACTAGTCTCTATTTCTGTAGAAAGAAACTAAGGCGCGAAATTTG 1558
DB 1445 CATAGTGTGATAGTACTAGTCTCTATTTCTGTAGAAAGAAACTAAGGCGCGAAATTTG 1504
QY 1559 TCTAAGATCACTTAACTAGGAAGTGGCAGAACTGATTTCTCCAGCCCTGGTGTGATTTGCT 1618
DB 1505 TCTAAGATCACTTAACTAGGAAGTGGCAGAACTGATTTCTCCAGCCCTGGTGTGATTTGCT 1564
QY 1619 CAGAGCTACGCTTGGTCCAGAACATCAAACTCCAAACCCCTGGGGAACAAACGACATGAA 1678
DB 1565 CAGAGCTACGCTTGGTCCAGAACATCAAACTCCAAACCCCTGGGGAACAAACGACATGAA 1624
QY 1679 TAAATGTATTTTAAACATC 1698
DB 1625 TAAATGTATTTTAAACATC 1644

RESULT 12

ADN95729

ID ADN95729 standard; DNA; 1645 BP.

XX AC ADN95729;

XX XX 01-JUL-2004 (first entry)

XX DE Human BEC/LEC-related gene sequence SeqID653.

XX growth; differentiation; blood endothelial cell; BEC;
XX lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
KW lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;


```
Db 1025 AGCTACAATCTGGACAAAAGTGTTCACATCACTAAACTCATCGCCACACCACCTGCTGC 1084
QY 1139 ATCAACCCCTCTCTGTATGCGTTTCTTGATGGGAATTTAGCAATACTCTGCGCGTGT 1198
Db 1085 ATCAACCCCTCTCTGTATGCGTTTCTTGATGGGAATTTAGCAATACTCTGCGCGTGT 1144
QY 1199 TTCCATCTCGGTAGTAACACCCCACTTCAACCCAGGGGCGACTGTCACAGGCAATCG 1258
Db 1145 TTCCATCTCGGTAGTAACACCCCACTTCAACCCAGGGGCGACTGTCACAGGCAATCG 1204
QY 1259 AGGGAAGAACCTTGACCATTTCCACCGAAGTGTAAACTAGCATCCACCAATGCAAGAAG 1318
Db 1205 AGGGAAGAACCTTGACCATTTCCACCGAAGTGTAAACTAGCATCCACCAATGCAAGAAG 1264
QY 1319 TAAACATGGAATTTTCATCTTTCTGCAATTAATTTTCATGTAATTTTCTACACATTTGTATAC 1378
Db 1265 TAAACATGGAATTTTCATCTTTCTGCAATTAATTTTCATGTAATTTTCTACACATTTGTATAC 1324
QY 1379 AAAATCGGATACAGGAAGAAAGGAGGAGGTGAGCTTAACATTTGCTAAGCACTGAATTTG 1438
Db 1325 AAAATCGGATACAGGAAGAAAGGAGGAGGTGAGCTTAACATTTGCTAAGCACTGAATTTG 1384
QY 1439 TCTCAGGCACCGTGAAGGCTCTTTACAAAAGTGAAGTCTCTTCGCTCTTACCACTTGTC 1498
Db 1385 TCTCAGGCACCGTGAAGGCTCTTTACAAAAGTGAAGTCTCTTCGCTCTTACCACTTGTC 1444
QY 1499 CATAGTGTGGATAGGACTAGTCTCAATTTCTCTGAGAAGAAACTAAGGCGCGGAATTTG 1558
Db 1445 CATAGTGTGGATAGGACTAGTCTCAATTTCTCTGAGAAGAAACTAAGGCGCGGAATTTG 1504
QY 1559 TCTAAGATCACCTAACTAGGAAGTGGCAGAACTGATTTCTCCAGCCCTGCTAGCATTTGCT 1618
Db 1505 TCTAAGATCACCTAACTAGGAAGTGGCAGAACTGATTTCTCCAGCCCTGCTAGCATTTGCT 1564
QY 1619 CAGAGCTACGCTTGGTCCAGAACATCAAACTCCAAACCTCGGGGACAAACGACATGAAA 1678
Db 1565 CAGAGCTACGCTTGGTCCAGAACATCAAACTCCAAACCTCGGGGACAAACGACATGAAA 1624
QY 1679 TAAATGTATTTTAAACATC 1698
Db 1625 TAAATGTATTTTAAACATC 1644

RESULT 14
AD575309
ID AD575309 standard; cDNA; 1645 BP.
XX
AC AD575309;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human CCR2 (chemokine (C-C motif) receptor-like 2) cDNA SeqID 1.
XX
KW gene; ss; inflammatory bowel disease; IBD; ulcerative colitis; CCR2;
KW GPCR receptor; chemokine (C-C motif) receptor-like 2; HCR; gene therapy;
KW antiinflammatory.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 203..1237
FT /*tag= a
FT /product= "CCR2 protein"
XX
XX WO2004083232-A2.
XX
XX 30-SEP-2004.
XX
XX 18-MAR-2004; 2004WO-GB001159.
XX
XX 20-MAR-2003; 2003GB-00006428.
XX
XX (OXAG-) OXAGEN LTD.
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XX
PI Pettipher R;
DR WPI; 2004-728453/71.
DR P-PSDB; ADS75310.
XX
PT Determining whether an individual is predisposed to inflammatory bowel
PT disease (i.e. ulcerative colitis) comprises identifying whether the
PT individual has a polymorphism in the CCR2 polynucleotide or protein.
XX
PS Claim 10; SEQ ID NO 1; 60pp; English.
XX
CC This invention relates to a novel method for determining whether an
CC individual is predisposed to inflammatory bowel disease (IBD); preferably
CC to ulcerative colitis. Specifically, it refers to the identification of
CC single nucleotide polymorphisms (SNPs) in the CCR2 polynucleotide or
CC encoded protein thereof, where CCR2 refers to the GPCR receptor
CC chemokine (C-C motif) receptor-like 2 protein that is also known as HCR.
CC The present invention describes methods for preventing or treating IBD,
CC as well as diagnosing a predisposition to the disease by use of probes,
CC primers and antibodies that can detect and amplify the CCR2 SNP regions.
CC Furthermore, it provides a screening assay for agents that can be used to
CC identify individuals with a genetic predisposition and in turn be used
CC for gene therapy purposes. The pharmaceutical compositions derived
CC therefrom exhibit an antiinflammatory activity. This polynucleotide
CC sequence is the human CCR2 cDNA of the invention. NOTE: This sequence
CC contains SNPs that are explicitly defined in individual DNA fragments
CC given in table 4 of the specification.
XX
SQ Sequence 1645 BP; 443 A; 383 C; 361 G; 458 T; 0 U; 0 Other;

Query Match 85.7%; Score 1455.2; DB 13; Length 1645;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1457; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 239 CCAGTGGGCGAGTCTGAAGATGGCCAAATTTACACGCTGGCACCAGAGGATGAATATGATGTC 298
Db 185 CCAAGGCGAGTCTGAGATGGCCAAATTTACACGCTGGCACCAGAGGATGAATATGATGTC 244
QY 299 CTCATAGAAGGTGAACCTGGAGAGCGATGAGGAGAGCAATGTGCAAGATATGACGCCAG 358
Db 245 CTCATAGAAGGTGAACCTGGAGAGCGATGAGGAGAGCAATGTGCAAGATATGACGCCAG 304
QY 359 GCACTCTCAGCCCGAGTGGTGGCATCACTCTGCTCTGCTGTGTTGTGATCGGTGCTCG 418
Db 305 GCACTCTCAGCCCGAGTGGTGGCATCACTCTGCTCTGCTGTGTTGTGATCGGTGCTCG 364
QY 419 GACAATCTCTGTTGTGCTTATCTGCTTAAATATAAAGGACTCAAAACGCGTGGAAAT 478
Db 365 GACAATCTCTGTTGTGCTTATCTGCTTAAATATAAAGGACTCAAAACGCGTGGAAAT 424
QY 479 ATCTATCTTAAACTTGGCAGTTTCTAACTTGTGTTCTTCTGCTTACCTGCCCTTCTGG 538
Db 425 ATCTATCTTAAACTTGGCAGTTTCTAACTTGTGTTCTTCTGCTTACCTGCCCTTCTGG 484
QY 539 GCTCATGCTGGGGCGATCCCATGTGTAATAATTTCTCATTTGACTGCTACTTCTGCGGCCG 598
Db 485 GCTCATGCTGGGGCGATCCCATGTGTAATAATTTCTCATTTGACTGCTACTTCTGCGGCCG 544
QY 599 TACAGTGAGACATTTTTTCAATTTGCCCTTCTGACTGTGCAAAAGGTACTAGTGTGTTTGCAC 658
Db 545 TACAGTGAGACATTTTTTCAATTTGCCCTTCTGACTGTGCAAAAGGTACTAGTGTGTTTGCAC 604
QY 659 AAGGCAACTTTTTTCTCAGCCAGGAGGGTGGCTGTGGGATCATTTACAAGTGTCTG 718
Db 605 AAGGCAACTTTTTTCTCAGCCAGGAGGGTGGCTGTGGGATCATTTACAAGTGTCTG 664
QY 719 GCATGGGTAACAGCAATTTCTGCCCACTTTGCTGTAATACGTTGTTTATAAACCTCAGATG 778
Db 665 GCATGGGTAACAGCAATTTCTGCCCACTTTGCTGTAATACGTTGTTTATAAACCTCAGATG 724
QY 779 GAAAGACCAGAAATACAAGTGTGCATTTAGCAGAACTCCCTTCTCCTGCCAGCTGATGACA 838
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Db 725 GAAGACAGAAATACAAGTGTGATTTAGCAGAACTCCCTTCCTGCGAGCTGATGACAA 784
QY TTCTGGAGCATTTTCTGACTTTAAATAAGCAATTTTCGTTCTTCTGCTCCCTATTT 898
Db 785 TTCTGGAGCATTTTCTGACTTTAAATAAGCAATTTTCGTTCTTCTGCTCCCTATTT 844
QY ATTTTACATTTCTCTATGTGCAAAATGAGAAAAACACTAAAGTTTCAGGGAGCAGAGTAT 958
Db 845 ATTTTACATTTCTCTATGTGCAAAATGAGAAAAACACTAAAGTTTCAGGGAGCAGAGTAT 904
QY AGCTTTTCAAGCTTGTGTTTTCGCAATATGATGATCTTCTCTGATGTTGGGCGCCCTAC 1018
Db 905 AGCTTTTCAAGCTTGTGTTTTCGCAATATGATGATCTTCTCTGATGTTGGGCGCCCTAC 964
QY AATATTGCAATTTTCTGCTGCTCACTTTCAAGAAACACTTTCTCCCTGAGTGAAGTCAAGAGC 1078
Db 965 AATATTGCAATTTTCTGCTGCTCACTTTCAAGAAACACTTTCTCCCTGAGTGAAGTCAAGAGC 1024
QY AGCTACAATCTGGACAAAAGTGTTCACATCACTAAACTCATCTGAGTGAAGTCAAGAGC 1138
Db 1025 AGCTACAATCTGGACAAAAGTGTTCACATCACTAAACTCATCTGAGTGAAGTCAAGAGC 1084
QY ATCAACCTCTCTGATGCTTTCTGATGAGCAATTTAGCAATACCTCTGCGCTGT 1198
Db 1085 ATCAACCTCTCTGATGCTTTCTGATGAGCAATTTAGCAATACCTCTGCGCTGT 1144
QY TTCCATCTGGTGTAGTAACACCCCTTCAACCCAGGGGAGTCTGCACAAAGCACAATCG 1258
Db 1145 TTCCATCTGGTGTAGTAACACCCCTTCAACCCAGGGGAGTCTGCACAAAGCACAATCG 1204
QY AGGGAAGAACTGACCACTTCCACCGAAGTGAATAGCATCCACCAATGCAAGAGAA 1318
Db 1205 AGGGAAGAACTGACCACTTCCACCGAAGTGAATAGCATCCACCAATGCAAGAGAA 1264
QY TAAACATGATTTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCT 1378
Db 1265 TAAACATGATTTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCT 1324
QY AAATCGATACAGGAAGAAAGGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1438
Db 1325 AAATCGATACAGGAAGAAAGGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1384
QY TCTCAGGACCGTGAAGGCTTTTACAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1498
Db 1385 TCTCAGGACCGTGAAGGCTTTTACAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1444
QY CATAGTGTGATAGGACTGCTCATTTCTGAGAGAAACTAAGGCGCGGAAATTTG 1558
Db 1445 CATAGTGTGATAGGACTGCTCATTTCTGAGAGAAACTAAGGCGCGGAAATTTG 1504
QY TCTAAGATCACTTAACTAGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1618
Db 1505 TCTAAGATCACTTAACTAGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1564
QY CAGAGCTACGCTTGTGTCAGAACTCAAACTCCAAACCTTGGGGCAAAACGACATGAAA 1678
Db 1565 CAGAGCTACGCTTGTGTCAGAACTCAAACTCCAAACCTTGGGGCAAAACGACATGAAA 1624
QY TAAATGATTTTAAACATC 1698
Db 1625 TAAATGATTTTAAACATC 1644

RESULT 15

ABD20648 ID ABD20648 standard; DNA; 143040 BP.

XX AC ABD20648;

XX AC ABD20648;

DT 29-JUL-2004 (first entry)

XX Human pulmonary and inflammatory target DNA #259.

XX

KW Human; antiseize; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; da.
XX Homo sapiens.
XX WO200285309-A2.
XX 31-OCT-2002.
XX 23-APR-2002; 2002WO-US013143.
XX 24-APR-2001; 2001US-0286036P.
XX (EPIC-) EPIGENESIS PHARM INC.
XX Nyce JW, Li Y, Sandraesgra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-093058/08.
XX Pharmaceutical composition for treating asthma, has antiseize
XX oligonucleotide containing less percentage of adenosine, targeted to
XX nucleic acids associated with lung airway or lung dysfunction, and
XX bronchodilating agent.
XX Claim 15; SEQ ID NO 12041; 763pp; English.
XX This invention describes a novel composition (a) a first active agent,
XX comprising oligonucleotides, effective for alleviating
XX bronchoconstriction, respiratory tract inflammation, allergies and
XX reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
XX surfactant depletion or hyposecretion, when administered to a mammal. The
XX oligonucleotides are derived from a gene encoding or regulating
XX expression of a target polypeptide associated with lung airway or lung
XX dysfunction or cancer and can be anti-sense to the corresponding mRNA.
XX The invention also describes a kit, that comprises: (a) a delivery
XX device, in separate containers, (b) the oligonucleotides, (c)
XX instructions for adding a carrier and for use of the kit. The composition
XX of the invention has antiallergic, antiinflammatory, antiasthmatic,
XX analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
XX beta-adrenergic agonist. The composition is useful for preventing or
XX treating a respiratory, lung or malignant disease. The administered
XX composition comprises oligo and is administered to reduce the production
XX or availability, or to increase the degradation of the target mRNA or to
XX reduce the amount of target polypeptide present in the lungs. The
XX pulmonary obstruction, and/or bronchoconstriction and/or lung
XX inflammation, allergies and/or surfactant hypoproduction are associated
XX with a disease or condition such as pulmonary vasoconstriction,
XX inflammation, allergies, asthma, impeded respiration, respiratory
XX distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
XX hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
XX transplantation rejection, pulmonary infections, bronchitis or cancer.
XX The reduced adenosine content of the anti-sense oligos corresponding to
XX thymidines present in the target RNA serves to prevent the breakdown of
XX the oligonucleotides into products that free adenosine into the system
XX e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
XX prevent any unwanted effects due to it

Sequence 143040 BP; 41190 A; 30113 C; 32394 G; 39343 T; 0 U; 0 Other;

Query Match 85.7%; Score 1455.2; DB 11; Length 143040;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1457; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 239 CCAGTGGGCGAGTCTGAAGATGCCCAATTAACGCTGGCAGCAGAGATGAATATGATGTC 298
Db 96624 CCACAGGGCGAGTCTGAAGATGCCCAATTAACGCTGGCAGCAGAGATGAATATGATGTC 96683

QY	299	CTCATAGAGGTGAACCTGAGAGCGCATGAGGCAGAGCAATGTGACAAAGTATGACGCCGAC	358
Db	96684	CTCATAGAAAGGTGAACCTGAGAGCGCATGAGGCAGAGCAATGTGACAAAGTATGACGCCGAC	96743
QY	359	GCACCTCTCAGCCAGCGTGGTGCACACCTCTGCTGTGTTGTGTGTGATCGGTGTCTTG	418
Db	96744	GCACCTCTCAGCCAGCGTGGTGCACACCTCTGCTGTGTTGTGTGTGATCGGTGTCTTG	96803
QY	419	GACAACTCTCCTGGTGTGCTTAATCTCTGTTAAATATAAAGAGCTCAAAACCGCTGGAAAT	478
Db	96804	GACAACTCTCCTGGTGTGCTTAATCTCTGTTAAATATAAAGAGCTCAAAACCGCTGGAAAT	96863
QY	479	ATCTATCTCTAAACTTGGCAGTTTCTAACTTGTGTTCTTCTGTTACCCCTGCCCTTCTGG	538
Db	96864	ATCTATCTCTAAACTTGGCAGTTTCTAACTTGTGTTCTTCTGTTACCCCTGCCCTTCTGG	96923
QY	539	GCTCATGCTGGGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTTTCGTGGGCCCTG	598
Db	96924	GCTCATGCTGGGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTTTCGTGGGCCCTG	96983
QY	599	TACAGTGAGACATTTTTCATTTGCCCTTCTGACTGTGCAAAAGTACTAGTGTTTTGTGCAC	658
Db	96984	TACAGTGAGACATTTTTCATTTGCCCTTCTGACTGTGCAAAAGTACTAGTGTTTTGTGCAC	97043
QY	659	AAGGGCACTTTTCTCAGCCAGGAGGAGGTGCCCTGTGGCATCATTTACAAGTGTCTTG	718
Db	97044	AAGGGCACTTTTCTCAGCCAGGAGGAGGTGCCCTGTGGCATCATTTACAAGTGTCTTG	97103
QY	719	GCATGGGTAAACGCCAATCTGGCCACTTTTGCCTGAATACGTGGTTTATAAAGCTCAGATG	778
Db	97104	GCATGGGTAAACGCCAATCTGGCCACTTTTGCCTGAATACGTGGTTTATAAAGCTCAGATG	97163
QY	779	GAAGACCAAGAAATACAAAGTGTGCAATTTAGCAGAACTCCCTTCTGTCAGCTGATGAGACA	838
Db	97164	GAAGACCAAGAAATACAAAGTGTGCAATTTAGCAGAACTCCCTTCTGTCAGCTGATGAGACA	97223
QY	839	TTCTGGAGCATTTTCTGACTTTTAAATGACATTTCCGTTCTTGTCTCCCTCTATTT	898
Db	97224	TTCTGGAGCATTTTCTGACTTTTAAATGACATTTCCGTTCTTGTCTCCCTCTATTT	97283
QY	899	ATTTTATACATTTCTCTATGTGCAATGAGAAAAACATAAGGTTTCAAGGAGCAGAGGTAT	958
Db	97284	ATTTTATACATTTCTCTATGTGCAATGAGAAAAACATAAGGTTTCAAGGAGCAGAGGTAT	97343
QY	959	AGCCTTTTCAAGCTTGTGTTTGTGCAATATGTTAGTGTCTTCTGATGTGGGGCCCTAC	1018
Db	97344	AGCCTTTTCAAGCTTGTGTTTGTGCAATATGTTAGTGTCTTCTGATGTGGGGCCCTAC	97403
QY	1019	AATATTGCAATTTTCTCTGTCCACTTTTCAAGAACACTTCTCCCTGAGTGACTGCAAGAGC	1078
Db	97404	AATATTGCAATTTTCTCTGTCCACTTTTCAAGAACACTTCTCCCTGAGTGACTGCAAGAGC	97463
QY	1079	AGCTACAATCTGGACAAAAGTGTTCACATCACTTAAACTCATGCCCCACCCACTGCTGC	1138
Db	97464	AGCTACAATCTGGACAAAAGTGTTCACATCACTTAAACTCATGCCCCACCCACTGCTGC	97523
QY	1139	ATCAACCCCTCTCCTGTATCGGTTTCTTGATGGGACATTTAGCAAAATACCTCTGCCGCTGT	1198
Db	97524	ATCAACCCCTCTCCTGTATCGGTTTCTTGATGGGACATTTAGCAAAATACCTCTGCCGCTGT	97583
QY	1199	TTCCATCTCGGTAGTAAACCCCACTTCAACCCAGGGGCGAGTCTGCAAGGGCACATCG	1258
Db	97584	TTCCATCTCGGTAGTAAACCCCACTTCAACCCAGGGGCGAGTCTGCAAGGGCACATCG	97643
QY	1259	AGGGAAGAACTCTGACCAATTTCCACCGAAGTGTAACTTAGCATCCACCAATGCAAGAGAA	1318
Db	97644	AGGGAAGAACTCTGACCAATTTCCACCGAAGTGTAACTTAGCATCCACCAATGCAAGAGAA	97703
QY	1319	TAAACATGGAATTTTCACTTTCTGCAATTAATTTTCACTGAATTTTCTACATTTGTATAC	1378
Db	97704	TAAACATGGAATTTTCACTTTCTGCAATTAATTTTCACTGAATTTTCTACATTTGTATAC	97763

Search completed: June 18, 2005, 16:00:34
Job time : 961 secs

QY	1379	AAAATCGGATACAGGAAGAAAGGAGGTGAGCTTAACATTTGCTTAAGCACTGAATTTG	1438
Db	97764	AAAATCGGATACAGGAAGAAAGGAGGTGAGCTTAACATTTGCTTAAGCACTGAATTTG	97823
QY	1439	TCTCAGGCACCGTGCAGGCTCTTTTACAAAAGTGAAGCTCCTTTGCGCTCCTTACCCTTGTG	1498
Db	97824	TCTCAGGCACCGTGCAGGCTCTTTTACAAAAGTGAAGCTCCTTTGCGCTCCTTACCCTTGTG	97883
QY	1499	CATAGTGTGGATAGGACTAGTCTCATTTCTCTGAGAAGAAAACCTAAGGCGCGGAAATTTG	1558
Db	97884	CATAGTGTGGATAGGACTAGTCTCATTTCTCTGAGAAGAAAACCTAAGGCGCGGAAATTTG	97943
QY	1559	TCTAAGATCACTTAACTAGGAAGTGGCAGAACTGATTTCTCCAGCCCTGCTAGCATTTGCT	1618
Db	97944	TCTAAGATCACTTAACTAGGAAGTGGCAGAACTGATTTCTCCAGCCCTGCTAGCATTTGCT	98003
QY	1619	CAGAGCCTACGCTTGGTCCAGAAACATCAAACTCCAAACCCCTGGGGACAAACGACATGAAA	1678
Db	98004	CAGAGCCTACGCTTGGTCCAGAAACATCAAACTCCAAACCCCTGGGGACAAACGACATGAAA	98063
QY	1679	TAAATGTATTTTAAACAATC	1698
Db	98064	TAAATGTATTTTAAACAATC	98083

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OM nucleic - nucleic search, using sw model

Run on: June 18, 2005, 14:53:56 ; Search time 5809 Seconds
(without alignments)

11126.378 Million cell updates/sec

Title: AF014958

Perfect score: 1698

Sequence: 1 AGACGGTTCAGAGATCCTCT.....TAAATGTATTTTAAACATC 1698

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	779.8	45.9	831	4	BI834559 603089767
2	763	44.9	880	4	BI819787 603041489
3	737.8	43.5	896	5	BQ892457 AGENCOURT
4	689	40.6	729	6	CD370587 UI-H-FTL-
5	688.4	40.5	716	7	CF147784 AGENCOURT
6	681.8	40.2	750	2	BE871331 601449442
7	646.4	38.1	1035	4	BG386374 602455580
8	629	37.0	720	6	CD520843 AGENCOURT
9	597.6	35.2	773	7	CO959196 AGENCOURT
10	581	34.2	581	5	BP300486 BP300486
11	573.4	33.8	576	5	BP295805 BP295805
12	553.4	32.6	581	5	BP300273 BP300273
13	545.8	32.1	573	2	AW300833 xk06907.x
14	520.4	30.6	547	1	AI343408 t96806.x
15	479	28.2	517	5	EX480211 DXFZp6861
16	469.8	27.7	475	2	BE465578 hu32605.x
17	462.2	27.2	2111	3	AK007808 Mus muscu
18	450.6	26.5	768	6	CD468404 LeukoS3_3
19	431.8	25.4	736	6	CD466140 LeukoS2_2
20	415.4	24.5	789	6	CD466479 LeukoN2_4
21	401	23.6	487	7	CR549318 DXFZp468A
22	398	23.4	683	6	CD535056 LeukoN5_3
23	396	23.3	424	2	AW293465 UI-H-BI2-
24	395.6	23.3	650	6	CD467795 LeukoS1_7

c	25	395.4	23.3	397	1	AI954582	AI954582 wx93902.x
	26	395	23.3	664	6	CD470054	LeukoS4_1
	27	394.8	23.3	673	6	CD466424	LeukoN2_4
	28	393.2	23.2	691	6	CD468594	LeukoS3_4
	29	391.8	23.1	654	6	CD466568	LeukoN2_7
	30	391.4	23.1	728	7	CO959203	AGENCOURT
	31	385	22.7	749	6	CD468632	LeukoS3_4
	32	382.6	22.5	724	6	CD469405	LeukoS2_3
	33	378.4	22.3	623	6	CD471186	LeukoS5_1
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	35	363.6	21.4	692	7	CN786392	4120380_B
c	36	363	21.4	369	1	AI288845	AI288845 qn24e01.x
	37	348.2	20.5	592	6	CD536762	LeukoN6_6
	38	345	20.3	592	6	CD471634	LeukoS6_4
	39	343.8	20.2	793	6	CD466229	LeukoN2_2
	40	341.6	20.1	578	6	CD465152	LeukoN1_2
	41	339.2	20.0	722	7	CK835230	4059514_B
	42	329.8	19.4	556	6	CD471194	LeukoS5_1
	43	329.8	19.4	564	6	CD467249	LeukoS1_3
	44	326.4	19.2	561	6	CD465288	LeukoN1_3
	45	325	19.1	564	6	CD472150	LeukoS6_1

ALIGNMENTS

BI834559 831 bp mRNA linear EST 04-OCT-2001
603089767F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5228561 5',
mRNA sequence.
ACCESSION BI834559
VERSION BI834559.1 GI:15946109
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE NIH-MGC http://mgs.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabbs@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLNL1575 row: f column: 18
High quality sequence stop: 813.

FEATURES

Location/Qualifiers
1..831
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/mol_type="mRNA"
/db_xref="taxon:9606"
/lab_host="DH10B"
/clone="IMAGE:5228561"
/clone_lib="NIH MGC 120"
/note="Organ: pooled pancreas and spleen; Vector: pcMV-SPORET6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (Socv) site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 45.9%; Score 779.8; DB 4; Length 831;

Best Local Similarity 99.3%; Pred. No. 1.6e-216;		Matches 825; Conservative 0; Mismatches 2; Indels 4; Gaps 4;	
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QY	183	CACAGCTCCCGGATGTGGGTCTGGAGGCTGCCGCCCTTCCCTGCAGGAGCTCAGCCCGAG	242
Db	120	CACAGCTCCCGGATGTGGGTCTGGAGGCTGCCGCCCTTCCCTGCAGGAGCTCAGCCCGAG	179
QY	243	TGGGCAGTCTGAAGATGGCCAAATTACACGCTGGCCACAGAGGATGAATATGATGTCTCTCA	302
Db	180	TGGGCAGTCTGAAGATGGCCAAATTACGCTGGCCACAGAGGATGAATATGATGTCTCTCA	239
QY	303	TAGAAGGTGAATGGAGAGCGATGAGGCAGAGCAATGTGACAAATATGACGCCCGAGCAC	362
Db	240	TAGAAGGTGAATGGAGAGCGATGAGGCAGAGCAATGTGACAAATATGACGCCCGAGCAC	299
QY	363	TCTCAGCCGAGCTGGTGCCATCACTCTGCTCTGCTGTGTTGTGATCGGTCTCTGGACA	422
Db	300	TCTCAGCCGAGCTGGTGCCATCACTCTGCTCTGCTGTGTTGTGATCGGTCTCTGGACA	359
QY	423	ATCTCTCGTGTGCTTATCCTCGTAAAAATATAAAGGACTCAAAACGGCGTGAAAAATATCT	482
Db	360	ATCTCTCGTGTGCTTATCCTCGTAAAAATATAAAGGACTCAAAACGGCGTGAAAAATATCT	419
QY	483	ATCTTTAAACTTTGGCAGTTTCTAACTGTGTTTCTTGTCTTACCTGCCCTTCTGGGCTC	542
Db	420	ATCTTTAAACTTTGGCAGTTTCTAACTGTGTTTCTTGTCTTACCTGCCCTTCTGGGCTC	479
QY	543	ATGCTGGGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTTCGTGGGCTGTACA	602
Db	480	ATGCTGGGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTTCGTGGGCTGTACA	539
QY	603	GTGAGACATTTTCAATTGGCTTCTGACTGTGCAAGGTACCTAGTGTTTTTGCAACAAG	662
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QY	663	GCAACTTTTCTCAGCAGGAGGGTGCCCTGTGGCATCATTTACAAGTGTCTCTGGCAT	722
Db	600	GCAACTTTTCTCAGCAGGAGGGTGCCCTGTGGCATCATTTACAAGTGTCTCTGGCAT	659
QY	723	GGGTAAACAGCA-TTCTGGCCACTTTTG-CCTGGAATACGTGGTTTATAAACCACAGATGGA	780
Db	660	GGGTAAACAGCA-TTCTGGCCACTTTTGCCCTGAATACGTGGTTTATAAACCACAGATGGA	719
QY	781	AGACCAAGAAATACAAGTGTGCATTTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATT	840
Db	720	AGACCAAGAAATACAAGTGTGCATTTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATT	779
QY	841	CTGGAGAGCATTTTCTGACTTTTAAAAATGAAATTTGGTTCTTGCTCTCC	891
Db	780	CTGGAGAGCATTTTCTGACTTTTAAAAATGAAATTTGGTTCTTGCTCTCC	830

RESULT 2	
BI819787	
LOCUS	880 bp mRNA linear EST 04-OCT-2001
DEFINITION	G03041489F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5182006 5' ,
	mRNA sequence.
ACCESSION	BI819787
VERSION	BI819787.1 GI:15931337
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE	1 (bases 1 to 880)

QY 559 CATGTGTAAATTTCTCATTTGAGCTGTACTTCTGTTGGGCTGTACAGTGAGACATTTTTCAA 618
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 Db 601 TTGCTTCTGACGTGTGCAAGGTACCTAGTGTGTTTTCACAAAGGCACTTTTCTCAGC 659
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 QY 679 CAGGAGGAGGTTGCCCTGT--GGCATCAATTACAAAGTGTCTGGCATGGGTAAACAGCCATTC 737
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 Db 660 CAGGAGGAGGTTGCCCTGTGGGCATCAATTACAAAGTGTCTGGCATGGGTAAACAGCCATTC 719
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 QY 738 TGGCCATTGTCCT--GAATACGTGTTTATAAACCCTCAGAT--GGAAGACCAAGAAATAC 793
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 Db 720 TGGCCATTGTCCT--GAATACGTGTTTATAAACCCTCAGAT--GGAAGACCAAGAAATAC 779
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 QY 794 AAGTGTGCATTTAGCAGACTCCCTTCTGCCAGCTGATGA---GACATTTCTGGAAGCA 849
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 Db 780 AAGTGTGCATTTAGCAGACTCCCTTCTGCCAGCTGATGA---GACATTTCTGGAAGCA 839
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 QY 850 TTTTCTGACTTTAAATGAACATTTTCGGTCTCTGCTCC 890
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 Db 840 TTTTCTGACTTTAAATGAACATTTTCGGTCTCTGCTACC 880
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RESULT 3

BQ892457 896 bp mRNA linear EST 16-AUG-2002
 LOCUS AGENCOURT_8415422 Lupeki_sympathetic_trunk Homo sapiens cDNA clone
 DEFINITION IMAGE:6192227 5', mRNA sequence.

ACCESSION

BQ892457

VERSION

BQ892457.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

NIH-MGC <http://mhc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM13593 row: 0 column: 12
 High quality sequence stop: 601.

FEATURES

source

1..896
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 /db_xref="taxon:9606"
 /clone="IMAGE:6192227"
 /sex="male"
 /tissue_type="sympathetic trunk"
 /dev_stage="adult, 16 yr"
 /lab_host="DH10B"
 /clone_lib="Lupeki sympathetic trunk"
 /note="Vector: PCW-SPOR16 (Life Technologies); Site 1:
 NotI; Site 2: SalI; cDNA made by oligo-dT priming.
 Directionally cloned using the following adaptors:
 5'-TCGACCCAGCGTCCG-3' and
 5'-GACTAGTCTTAGTCGAGCGGCCCT(15)-3'. Size selected >
 1 kb for average insert length 1.9 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine); available through Life

Technologies."

ORIGIN
 Query Match 43.5%; Score 737.8; DB 5; Length 896;
 Best Local Similarity 96.5%; Pred. No. 3.4e-204;
 Matches 850; Conservative 0; Mismatches 22; Indels 9; Gaps 9;
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 Db 1 ACCAGAGGATGAATATGATGTCTCTATAGAAGGTGAACCTGGAGAGGATGAGGACAGCA 60
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 QY 337 ATGTGCAAGATGAGCGCCAGGCACTCTCAGCCAGCTGTGTCCTCATCTCTGCTCTGC 396
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 Db 61 ATGTGCAAGATGAGCGCCAGGCACTCTCAGCCAGCTGTGTCCTCATCTCTGCTCTGC 120
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 QY 397 TGTGTTTGTGATCGGTGCTCTGACAAATCTCTCTGGTGTGCTTATCTCTGTAATAATAA 456
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 Db 121 TGTGTTTGTGATCGGTGCTCTGACAAATCTCTCTGGTGTGCTTATCTCTGTAATAATAA 180
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 QY 457 AGGACTCAAAACGCTGGAAATATATCTATCTCTTAAACTTTGGCAGTTTCTAACTTGTGTTT 516
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 Db 181 AGGACTCAAAACGCTGGAAATATATCTATCTCTTAAACTTTGGCAGTTTCTAACTTGTGTTT 240
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 QY 517 CTTGCTTACCTGCGCTTCTGGCTCATCTCTGGGGGATGCCATGTGTAATAATCTCAT 576
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 QY 577 TGGAGCTGACTTCTGGGCTCTGACAGTGAGACATTTTCAATTTGCTTCTGACTGTGCA 636
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 Db 361 AAGGTACCTAGTGTGTTTTTGCAAGGGCAATTTTTCTCAGCCAGGAGGGTGGCCTG 420
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 Db 421 TGGCATCAATTACAAGTGTCTGGCATGGGTAAACAGCCATTTCTGGCCATTTTGCCTGAATA 480
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 Db 541 CTTCTGCGCAGCTGATGAGACATTTCTGGAAGCATTTTCTGACTTTTAAAAATGAACATTTT 600
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 QY 877 GGTCTTGTGCTT-CCCCCTATTTTATTTTACATTTTCTCTATGTGCAAAATGAGAAAAACAC 935
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 QY 936 TAAAGTTTCA-GGGAGCAGAGGTATAGCCTTTTC-AGCTTGTGTTTGTGCCAT-AATGGTAG 992
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RESULT 4

CD370587/c

LOCUS

UI-H-FTI-bkc-j-11-0-UI.81

DEFINITION

UI-H-FTI-bkc-j-11-0-UI 3', mRNA sequence.

729 bp mRNA linear EST 05-AUG-2004

UI-H-FTI-bkc-j-11-0-UI.81 NCI CGAP FPI Homo sapiens cDNA clone

UI-H-FTI-bkc-j-11-0-UI 3', mRNA sequence.

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ACCESSION CD370587
VERSION CD370587.1 GI:31154677
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1. (bases 1 to 729)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
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                /clone_lib="NCI-CGAP FT1"
                /note="Organ: Lung; Vector: pTT73-Pac (Pharmacia) with a
                modified polylinker; Site 1: EcoR I; Site 2: Not I;
                NCI CGAP FT1 is a normalized cDNA library constructed from
                a pool of 81 RNA samples from Alveolar Macrophages
                challenged with different treatments. The mRNA samples
                were a mixture of these conditions (times refer to
                incubations following isolation by bronchoalveolar lavage)
                (some normal donor macrophages were cultured in some of
                the conditions). Other donor macrophages in different
                conditions). The mRNA samples were pooled for library
                construction. Control 0 hours; Control 3 hours; Control 24
                hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
                PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
                moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
                moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
                vector (Ad5 CMV egfp), moi 500, 3 hours; Adenoviral vector
                (Ad5 CMV egfp), moi 500, 24 hours; wt adenovirus moi 500,
                3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
                3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
                hours; wt adenovirus + LPS 24 hours. The library was
                normalized according to Bonaldo, Lennon and Soares, Genome
                Research, 6:791-806, 1996. First strand cDNA synthesis was
                primed with an oligo-dT primer containing a Not I site.
                Double stranded cDNA was ligated to an EcoR I adaptor,
                digested with Not I, and cloned directionally into
                pTT73-Pac vector. The oligonucleotide used to prime the
                synthesis of first-strand cDNA contains a library tag
                sequence that is located between the Not I site and the
                (dT)18 tail. The sequence tag for this library is
                GGCCATGCGG. The tissue was provided by Dr. Gary W.
                Hunninghake of the University of Iowa.
                TAG LIB=UI-H-FT1
                TAG_SEQ=GGCCATGCGG"

ORIGIN
Query Match 40.6%; Score 689; DB 6; Length 729;
Best Local Similarity 99.7%; Pred. No. 6.3e-190;
Matches 711; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
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Db 729 TGACTGTGCAAGGTACCTAGTG-TTTTGCACAGGGCAAC-TTTTCTCAGCCAGGAGGA 672
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Db 671 GGGTGCCCTGTGGCATCATTAACAAGTGTCTGGCATGGGTAAACGCCAATCTTGGGCACATT 612
QY 747 TGCCTGAATACGTGGTTTATAAACCCTCAGATGGAGACACAGAAATACAAAGTGTGCATTTA 806
Db 611 TGCCTGAATACGTGGTTTATAAACCCTCAGATGGAGACACAGAAATACAAAGTGTGCATTTA 552
QY 807 GCAGAACTCCCTTCTCGCCAGCTGATGAGACATTCCTGAAGCATTTTCTGACTTTAAAAAA 866
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QY 987 TGGTAGTCTTCTTCTGATGTGGGCGCCCTACAATATTGCAATTTTCTGTCCTCACTTTCA 1046
Db 371 TGGTAGTCTTCTTCTGATGTGGGCGCCCTACAATATTGCAATTTTCTGTCCTCACTTTCA 312
QY 1047 AAGAACACTTCTCCCTGAGTGACGTGCAAGAGCAGCTACAATCTGTGCAAAAAGTGTTCACA 1106
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QY 1107 TCACCTAACTATCGCCACACCCCACTCTCGATCAGCCCTCTCTGTATGCGTTTCTTG 1166
Db 251 TCACCTAACTATCGCCACACCCCACTCTCGATCAGCCCTCTCTGTATGCGTTTCTTG 192
QY 1167 ATGGGACATTTAGCAAAATACCTCTGCCCTGTGTTTCCATCTGGTAGTAACACCCCACTTC 1226
Db 191 ATGGGACATTTAGCAAAATACCTCTGCCCTGTGTTTCCATCTGGTAGTAACACCCCACTTC 132
QY 1227 AACCAGGGGCGAGTCTGCAACAAGCAGCATCGAGGGAAGAACCTGACCATTCACCGAAG 1286
Db 131 AACCAGGGGCGAGTCTGCAACAAGCAGCATCGAGGGAAGAACCTGACCATTCACCGAAG 72
QY 1287 TGTAACCTAGCATCCACCAATGCAAGAGATTAACATGATTTTCATCTTT 1339
Db 71 TGTAACCTAGCATCCACCAATGCAAGAGAAATAACATGATTTTCATCTTT 19

RESULT 5
LOCUS CF147784
DEFINITION AGENCOURT_14740191 NIH_MGC_145 Homo sapiens cDNA clone
IMAGE:6971947 5', mRNA sequence.
ACCESSION CF147784
VERSION CF147784.1 GI:33244052
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1. (bases 1 to 716)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

```


Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: IRB102 row: f column: 06
 High quality sequence stop: 634.
 Location/Qualifiers

FEATURES

1. 716
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 /notes="vector: pCDNA3.1; Site 1: varies by clone; Site 2: varies by clone; ORFs were PCR-amplified and cloned into pCDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmnI/XhoI-3', 5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRB1.presv.dat
 a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 40.5%; Score 688.4; DB 7; Length 716;
 Best Local Similarity 98.9%; Pred. No. 9.4e-190;
 Matches 703; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
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 Db 3 GGCAGTCTGAAGTGGCCAAATACAGCTGGCACCAGAGGATGAATATGCTCTCAT 62
 304 AGAAGTGAACCTGGAGCGCATGAGCAGAGCAATGTGCAAGTATGACGCCAGGCAC 363
 Db 63 AGAAGTGAACCTGGAGCGCATGAGCAGAGCAATGTGCAAGTATGACGCCAGGCAC 122
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 604 TGAGACATTTTCAATTTGCTTCTGACTGTGCAAGGTACCTAGTGTGTTTGCACAAGG 663
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 664 CAACCTTTTCTCAGCAGAGGAGGGTGCCTGTGGCATCATTTACAAAGTCTCTGGCATG 723
 Db 423 AAACCTTTTCTCAGCAGAGGAGGGTGCCTGTGGCATCATTTACAAAGTCTCTGGCATG 482
 724 GGTAAACAGCCATTTCTGGCCATTTTGCTGGAATACGTGGTTTATPAAACCTCAGATGGAAGA 783
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 Db 543 CCAGAAATACAGTGTGCAATTTAGCAGAACTCCCTTCCTGCCAGCTGTAGACATTCCTG 602
 844 GAAGCATTTTCTGACATTTAAATGAACATTTGGTTCCTGCTCCCTTATTTATTTT 903
 Db 603 GAAGCATTTTCTGACATTTNAAATGAACATTTTGGTTCCTGCTCCCTTATTTATTTAT 662

904 TACATTTCTCTATGTGCAATGAGAAAAACACTAAGGTTTCAGGAGCAGAG 954
 Db 663 TACATTTCTCTATGTGCAATGAGAAAAACACT-AGGTTTCAGGAGCAGAG 712
 RESULT 6
 BE871331 750 bp mRNA linear EST 20-OCT-2000
 LOCUS 601449442F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853378 5',
 DEFINITION mRNA sequence.
 ACCESSION BE871331
 VERSION BE871331.1 GI:10320107
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 750)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLAM9577 row: c column: 11
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 Location/Qualifiers
 1. 750
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 /clone_lib="NIH_MGC_65"
 /note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.8 kb. Library constructed by Life Technologies."

ORIGIN

Query Match 40.2%; Score 681.8; DB 2; Length 750;
 Best Local Similarity 96.7%; Pred. No. 8.2e-188;
 Matches 728; Conservative 0; Mismatches 22; Indels 3; Gaps 3;
 47 TTTATTTCAAGTTGGTCCCTGAGCTCGGTGAGTGGGGGGGTAGAGCCACGAGGGGAATCA 106
 Db 1 TTTATTTCAAGTTGGTCCCTGAGCTCGGTGAGTGGGGGGGTAGAGCCACGAGGGGAATCA 60
 107 ACAGTGGTTTCTCGTGCCCTCAGGGTCAGGAGCAGTCTGATCAAAAGGAGGCATCCAC 166
 Db 61 ACAGTGGTTTCTCGTGCCCTCAGGGTCAGGAGCAGTCTGATCAAAAGGAGGCATCCAC 120
 167 TGTCCGGGCCAATTCACAGCTCCCGATGCTGGGTCTGGAGGCTGCGCCCTTCCCCTG 226
 Db 121 TGTCCGGGCCAATTCACAGCTCCCGATGCTGGGTCTGGAGGCTGCGCCCTTCCCCTG 180
 227 CAGGAGCTCAGCCCAAGTGGCAGTCTGAAGATGGCCAATTACCGCTGGCACCAGAGGAT 286
 Db 181 CAGGAGCTCAGCCCAAGTGGCAGTCTGAAGATGGCCAATTACACGCTGGCACCAGAGGAT 240
 287 GAATATGATGCTCTCATAGAAGGTGAATGGAGAGCGATGAGCAGAGCAATGTGCAAG 346
 Db 241 GAATATGATGCTCTCATAGAAGGTGAATGGAGAGCGATGAGCAGAGCAATGTGCAAG 300
 347 TATAGCCCCAGGCACCTCTCAGCCAGCTGGTGCCATCACTCTGCTCTGCTGTTTGTG 406

Db 301 TATGAGCCCGCAGCACTCTCAGCCAGCTGGTGCCATCACTCTGCTCTGCTG-TTGTG 359
 QY 407 ATCGGTGTCCTGGA CAATCTCTGTTGTGCTTATCTCTGGTAAATATATAAGGACTCAAA 466
 Db 360 ATCGGTGTCCTGGA CAATCTCTGTTGTGCTTATCTCTGGTAAATATATAAGGACTCAAA 419
 QY 467 CGGTGGGAAATATCTATCTCTTAACTTGGGAGTTTCTAACTGTTGTTCTTGTCTTACC 526
 Db 420 CGGTGGGAAATATCTATCTCTTAACTTGGGAGTTTCTAACTGTTGTTCTTGTCTTACC 479
 QY 527 CTGCCCCTCTGCGCTCATCTCTGGGGCGATCCCATGTGTAAATTTCTCAATGGACTGTAC 586
 Db 480 CTGCCCCTCTGCGCTCATCTCTGGGGCGATCCCATGTGTCAATTTCTCA-TGGACTGTAC 538
 QY 587 TTCTGGGGCTGTACAGTGAGACATTTTTCATTTGCTTCTGACTGTGTGCAAAAGTACCTTA 646
 Db 539 TTCTGGGGCTGTACAGTGAGACATTTTTCATTTGCTTCTGACTGTGTGCAAAAGTACCTTA 598
 QY 647 GTGTTTTTGCACAGGCACTTTTCTCAGCCAGGAGGGTGCCCTGTGGCATCATTT 706
 Db 599 GTG-TTTTGCACAGGCACTTTTCTCAGCCAGGAGGGTGCCCTGTGGCATCATTT 657
 QY 707 ACAAGTGTCTCTGGCATGGTAACAGCACTTCTGGCACTTTTGCCTGAATACGTTGGTTTAT 766
 Db 658 ACAAGTGTCTGGCATGGTAACAGCACTTCTGGCACTTTTGCCTGAATACGTTGGTTTAT 717
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 Db 718 AAACCTCAGATGGAAGACAGCAATCCAGTGT 750

RESULT 7
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 LOCUS 60245580F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4584043 5',
 DEFINITION mRNA sequence.

ACCESSION BG386374
 VERSION BG386374.1 GI:13279820
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1035)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: NIH Intramural Sequencing Center
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLM1308 row: o column: 20
 High quality sequence stop: 626.
 Location/Qualifiers

FEATURES
 source

1..1035
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 /clone="IMAGE:4584043"
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 /clone_lib="NIH MGC 15"
 /note="Organ: colon; Vector: pOTB7; Site: 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dr priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACACAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN	Query Match	Best Local Similarity	Score	DB 4;	Length
Matches	720;	Conservative	0;	Mismatches	31;
				Indels	5;
				Gaps	5;
QY	19	CTGAGGCGCTGGGGAGCTTTTGTAGTACTTATTTTCAAGTTGGTCCCTGAGCTCGGTGAGT	78		
Db	2	CTGAGGCGCTGGGGAGCTTTTGTAGTACTTATTTTCAAGTTGGTCCCTGAGCTCGGTGAGT	61		
QY	79	GGGGCGGCTAGAGCCACCCAGGGGAATCAACAGTGGTTTCTGTCGCCCTCAGGGTCAGGA	138		
Db	62	GGGGCGGCTAGAGCCACCA-GGGAAATCAACAGTGGTTTCTGTCGCCCTCAGGGTCAGGA	120		
QY	139	CGAGTCTGATCAAAAGGAGGGCATCCACTGTCCGGGGCCATTTCCACAGCTCCCGGATGC	198		
Db	121	CGAGTCTGATCAAAAGGAGGGCATCCACTGTCCGGGGCCATTTCCACAGCTCCCGGATGC	180		
QY	199	TGGGTCTGGAGGCTCGGCCCTTCCCTCTGAGGAGCTCAGCCAGTGGGAGTCTGAA-GA	257		
Db	181	TGGGTCTGGAGGCTCGGCCCTTCCCTCTGAGGAGCTCAGCCAGTGGGAGTCTGAA-CGA	240		
QY	258	TGGCCAAATTACACGCTGGCACAGAGGATGAATATGATGTCTCTATAGAGGTGAACCTGG	317		
Db	241	TGGCCAAATTACACGCTGGCACAGAGGATGAATATGATGTCTCTATAGAGGTGAACCTGG	300		
QY	318	AGAGCGATGAGGCGAGCAATGTGACAAAGTATGAGCCCGCAGGCACTCTCAGCCAGCTGG	377		
Db	301	AGAGCGATGAGGCGAGCAATGTGACAAAGTATGAGCCCGCAGGCACTCTCAGCCAGCTGG	360		
QY	378	TGCCATCACTCTGCTCTGCTGTTTGTGATCGGTGTCTCTGGACAATCTCTGTTGTGTC	437		
Db	361	TGCCATCACTCTGCTCTGCTGTTTGTGATCGGTGTCTCTGGACAATCTCTGTTGTGTC	420		
QY	438	TTATCTCTGTAATAATAAAGGACTCAAAACGGTCGGAATAATCTATCTTCTAAACTGG	497		
Db	421	TTATCTCTGTAATAATAAAGGACTCAAAACGGTCGGAATAATCTATCTTCTAAACTGG	480		
QY	498	CAGTTTCTAACTGTGTTTCTTGTCTTACCTTCCCTTCTGGGCTCATGCTGGGGCGATC	557		
Db	481	CAGTTTCTAACTGTGTTTCTTGTCTTACCTTCCCTTCTGGGCTCATGCTGGGGCGATC	540		
QY	558	CAATGTGTAATAATCTCAATTGAGCTGTTGCTGGGCTGTACAGTGAGACATTTTCA	617		
Db	541	CAATGTGTAATAATCTCAATTGAGCTGTTGCTGGGCTGTACAGTGAGACATTTTCA	600		
QY	618	ATTGCTTCTGACTGTGCAAAAGGTACCT-AGTGTGTTTTCACCAAGGCACTTTTCTCA	676		
Db	601	ATTGCTTCTGACTGTGCAAAAGGTACCT-AGTGTGTTTTCACCAAGGCACTTTTCTCA	660		
QY	677	GCCAGGAGGAGGTGCCCTGTGGCATCATTTACA-AGTGTCTCTGGCATGGGTAAACCCAT	735		
Db	661	GCCAGGAGGAGGTGCCCTGTGGCATCATTTACAAGTGTCTCTGGCATGGGTAAACCCAT	720		
QY	736	TC-TGGCCCACTTTGCTGCTGAATACGTTGTTTATAAC	770		
Db	721	TCTTGGCCCACTTTGCTGCTGAATTCGGTGGTTATAAGC	756		

RESULT 8
 CD520843

LOCUS AGNCOURT_14369985 NIH_MGC_191 Homo sapiens cDNA clone
 DEFINITION IMAGE:30409698 5', mRNA sequence.

ACCESSION CD520843
 VERSION CD520843.1 GI:31452561

KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.


```
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yezukui@ims.u-tokyo.ac.jp.

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ORIGIN
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Best Local Similarity 99.7%; Pred. No. 4.4e-156;
Matches 574; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCTTCAGAGATCCTCTGGAGGCTGGGGAGCTTTTGAGTACTTTTATTTTCAGTTGGTC 62
Db |||||
QY 63 CCTGAGCTCGTCAGTGGGGCGGTAGAGCCACAGGGGAATCAACAGTGGTTCTCGTG 122
Db |||||
QY 61 CCTGAGCTCGTCAGTGGGGCGGTAGAGCCACAGGGGAATCAACAGTGGTTCTCGTG 120
Db |||||
QY 123 CCCTCAGGCTCAGGAGCAGTCTGATCAAAAGAGGGCATCCACTGTCCGGGGCCATTCC 182
Db |||||
QY 121 CCCTCAGGCTCAGGAGCAGTCTGATCAAAAGAGGGCATCCACTGTCCGGGGCCATTCC 180
Db |||||
QY 183 CACAGCTCCCGGATGCTGGGTCTGGAGGCTGCGCCCTTCCCTGCAGGAGCTCAGCCAG 242
Db |||||
QY 181 CACAGCTCCCGGATGCTGGGTCTGGAGGCTGCGCCCTTCCCTGCAGGAGCTCAGCCAG 240
Db |||||
QY 243 TGGGCACTCTGAAGTGGCCAAATACAGCTGCAGGAGGATGATATGATGTCCTCA 302
Db |||||
QY 241 TGGGCACTCTGAAGTGGCCAAATACAGCTGCAGGAGGATGATATGATGTCCTCA 300
Db |||||
QY 303 TAGAAGGTGAATGGAGAGCGATGAGCAGAGCAATGTGACAAAGTATGAGCCCGAGCAC 362
Db |||||
QY 301 TAGAAGGTGAATGGAGAGCGATGAGCAGAGCAATGTGACAAAGTATGAGCCCGAGCAC 360
Db |||||
QY 363 TCTCAGCCAGCTGGTGCCATCACTCTGCTCTCTGTGTTGTGATCGGTGCTCTGGACA 422
Db |||||
QY 361 TCTCAGCCAGCTGGTGCCATCACTCTGCTCTCTGTGTTGTGATCGGTGCTCTGGACA 420
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QY 423 ATCTCTGCTGTGCTTATCTCTGTTAAATATATAAGGACTCAACCGGTGGAAAAATATCT 482
Db |||||
QY 421 ATCTCTGCTGTGCTTATCTCTGTTAAATATATAAGGACTCAACCGGTGGAAAAATATCT 480
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QY 483 ATCTCTAAACTGGCAGTTTCTAACTTGTTGTTCTTGTACCTCGCCCTCTCGGGCTC 542
Db |||||
QY 481 ATCTCTAACTGGCAGTTTCTAACTTGTTGTTCTTGTACCTCGCCCTCTCGGGCTC 540
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QY 543 ATGCTGGGGCGGATCCCATGTGPAAAATTCTCATG 578
Db |||||
QY 541 ATGCTGGGGCGGATCCCATGTGTAATAATTCTCATG 576
Db |||||

RESULT 12
BP300273 Sugano cDNA library, macrophage Homo sapiens cDNA clone
LOCUS MPE00730, mRNA sequence.
DEFINITION BP300273.1 GI:52229233
ACCESSION BP300273 Homo sapiens (human)
VERSION BP300273.1
KEYWORDS EST.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 581)
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,

TITLE
JOURNAL
COMMENT

Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yezukui@ims.u-tokyo.ac.jp.

FEATURES
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Best Local Similarity 99.8%; Pred. No. 3.2e-150;
Matches 554; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGACGCTTCAGAGATCCTCTGGAGGCTGGGGAGCTTTTGAGTACTTTTATTTTCAGTTGG 60
Db |||||
QY 27 AGACGCTTCAGAGATCCTCTGGAGGCTGGGGAGCTTTTGAGTACTTTTATTTTCAGTTGG 86
Db |||||
QY 61 TCCTCAGCTCCGTGAGTGGGGCGGTAGAGCCACAGGGGAATCAACAGTGGTTCTCG 120
Db |||||
QY 87 TCCTCAGCTCCGTGAGTGGGGCGGTAGAGCCACAGGGGAATCAACAGTGGTTCTCG 146
Db |||||
QY 121 TGCCCCCTCAGGCTCAGGAGCAGTCTGATCAAAAGAGGGCATCCACTGTCCGGGGCCATT 180
Db |||||
QY 147 TGCCCCCTCAGGCTCAGGAGCAGTCTGATCAAAAGAGGGCATCCACTGTCCGGGGCCATT 206
Db |||||
QY 181 CCCACAGCTCCCGGATGCTGGGTCTGGAGGCTGCGCCCTTCCCTGCAGGAGCTCAGCCC 240
Db |||||
QY 207 CCCACAGCTCCCGGATGCTGGGTCTGGAGGCTGCGCCCTTCCCTGCAGGAGCTCAGCCC 266
Db |||||
QY 241 AGTGGGCACTCTGAAGTGGCCAAATACAGCTGCAGGAGGATGATATGATGTCCT 300
Db |||||
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Db |||||
QY 301 CATAGAAGTGAATCTGGAGAGCGATGAGCAGAGCAATGTGACAAAGTATGACGCCAGGC 360
Db |||||
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Db |||||
QY 361 ACTCTCAGCCAGCTGGTGCCATCACTCTGCTCTGCTGTGTTGTGATCGGTGCTCTGGA 420
Db |||||
QY 387 ACTCTCAGCCAGCTGGTGCCATCACTCTGCTCTGCTGTGTTGTGATCGGTGCTCTGGA 446
Db |||||
QY 421 CAATCTCTGGTTGCTTATCTCTGTTAAATATATAAGGACTCAACCGGTGGAAAAATAT 480
Db |||||
QY 447 CAATCTCTGGTTGCTTATCTCTGTTAAATATATAAGGACTCAACCGGTGGAAAAATAT 506
Db |||||
QY 481 CTATCTCTAAACTTGGCAGTTTCTAACTTGTTGTTCTTGTACCTCGCCCTCTCGGGC 540
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QY 507 CTATCTCTAAACTTGGCAGTTTCTAACTTGTTGTTCTTGTACCTCGCCCTCTCGGGC 566
Db |||||
QY 541 TCATGCTGGGGCGA 555
Db |||||
QY 567 TCATGCTGGGGCGA 581
Db |||||

RESULT 13
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LOCUS AW300833
DEFINITION xk06g07.x1 NCI CGAP Col9 Homo sapiens cDNA clone IMAGE:2665980 3,
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ACCESSION AW300833
VERSION AW300833.1 GI:6710510
KEYWORDS EST.
SOURCE Homo sapiens (human)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 573)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Meskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D. Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christina Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP
founded through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 401.
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/issue_type="moderately differentiated adenocarcinoma"
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/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Normalized to Cot 50. Average insert size 1.32Kb.
Normalized version of NCI CGAP_Col8. Library constructed
by Life Technologies."

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DB 573 CACTGCTGCATCAACCTCTCCTGTATGCGTTCTTGATGGACATTTAGCAATACCT 514
QY 1189 CTGCCCTCTTTCCATCTCGGTAGTAACACCCACATTCACCCAGGGGCGAGTCTGCACA 1248
DB 513 CTGCCCTCTTTCCATCTCGGTAGTAACACCCACATTCACCCAGGGGCGAGTCTGCACA 454
QY 1249 AGGCACATCGAGGAGAACCTGACCATTCACCGAAGTGTAACTAGCATCCACCAAT 1308
DB 453 AGGCACATCGAGGAGAACCTGACCATTCACCGAAGTGTAACTAGCATCCACCAAT 394
QY 1309 GCAAGAAGATAAATCGGATGATTTTCATCTTTCTGCAATTTATCATGTAATTTCTACAC 1368
DB 393 GCNAGAAGATAAATCGGATGATTTTCATCTTTCTGCAATTTATCAATGTAATTTCTACAC 334
QY 1369 ATTTGTATACAAATCGGATACAGGAAGAAAGGGAGAGGTGAGCTAAACATTTGTGTAAGC 1428
DB 333 ATTTGTATACAAATCGGATACAGGAAGAAAGGGAGAGGTGAGCTAAACATTTGTGTAAGC 274
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DB 273 ACTGAATTTGCTCAGGACCGTGCAGGCTCTTTTACAAACGTGAGCTCTTCGCTCCCT 214
QY 1489 ACCACTTGTCCATAGTGTGGATAGGACTAGTCTCATTTCTCTGAGAAGAAATCTAGGGG 1548
DB 213 ACCACTTGTCCATAGTGTGGATAGGACTAGTCTCATTTCTCTGAGAAGAAATCTAGGGG 154
QY 1549 CGGAAATTTGTCTAAGATCACTTAACCTAGGAAGTGGCAGAACTGATTTCTCCAGCCCTGT 1608
DB 153 CGGAAATTTGTCTAAGATCACTTAACCTAGGAAGTGGCAGAACTGATTTCTCCAGCCCTGT 94
QY 1609 AGCATTTGCTCAGAGCTAGCTTGGTCCAGAACATCAAACTCCAAACCTCGGGACAAA 1668

Db 93 AGCATTTGCTCAGACCTTACGCTTGGTTCAGAACATCAAACTCCAAACCTCGGGACAAA 34
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Db 33 CGACATGAATAAATGATTTTAAACATC 4
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ACCESSION AI343408
VERSION AI343408.1 GI:4080614
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 547)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution Information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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High quality sequence stop: 442.
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modified Polylinker; Site 1: Not I; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI-CGAP Col6 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 30.6%; Score 520.4; DB 1; Length 547;
Best Local Similarity 99.3%; Pred. No. 1.5e-140;
Matches 543; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
QY 1154 TATGCGTTTCTTGATGGACATTTAGCAAAATACCTCTGCCGCTGTTTCCATCTGGTAGT 1213
DB 547 TATGCGTTTCTTGATGGACATTTAGCAAAATACCTCTGCCGCTGTTTCCATCTGGTAGT 488
QY 1214 AACACCCCACCTTCAACNCAGGGGGGAGTCTGCAACAGGCATCGAGGAGAACCCCTG 428
DB 487 AACACCCCACCTTCAACNCAGGGGGGAGTCTGCAACAGGCATCGAGGAGAACCCCTG 428
QY 1272 ACCATTCCACCCAGGTGTAACCTAGCATCCACAAATGCAAGAAGATAAATGATTT 1331
DB 427 ACCATTCCACCCAGGTGTAACCTAGCATCCACAAATGCAAGAAGATAAATGATTT 368

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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(without alignments)
9079.732 Million cell updates/sec

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Perfect score: 1698
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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5: /cgn2_6/prodata/1/ina/PCTUS COMB.seq.*
6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1448.2	85.3	1547	4	US-10-039-659A-11
2	1268	74.7	1270	4	US-09-016-434-756
3	981.2	57.8	1050	3	US-08-681-192-1
4	597.8	35.2	620	4	US-09-023-655-308
5	233	13.7	1059	3	US-09-517-605-8
6	233	13.7	1059	4	US-08-771-276-19
7	230.6	13.6	1059	3	US-08-724-984A-3
8	230.6	13.6	1225	4	US-09-023-655-967
9	230.6	13.6	1376	3	US-09-087-232A-12
10	230.6	13.6	1376	4	US-09-016-434-1104
11	230.6	13.6	1376	4	US-09-796-202-2
12	230.6	13.6	1414	4	US-09-502-783A-1
13	230.6	13.6	1414	4	US-09-502-784A-1
14	230.6	13.6	1414	4	US-09-339-912A-1
15	230.6	13.6	1414	4	US-09-195-662A-1
16	230.6	13.6	1477	3	US-08-833-752-2
17	230.6	13.6	1477	4	US-09-938-719-2
18	230.6	13.6	1477	4	US-09-939-226B-2
19	230.6	13.6	3383	3	US-08-861-105-13
20	230.6	13.6	3383	3	US-08-575-967A-1
21	230.6	13.6	3383	4	US-09-023-655-951
22	230.6	13.6	3383	4	US-08-771-276-1
23	230.6	13.6	5674	3	US-09-293-170-3
24	239	13.5	1059	4	US-09-826-509-476
25	239	13.5	1071	3	US-09-087-232A-14
26	225.8	13.3	1414	3	US-08-466-343D-1
27	196.6	11.6	1065	3	US-08-847-296B-2

28	196.6	11.6	1139	4	US-08-375-199B-3
29	196.6	11.6	1193	4	US-08-720-565-3
30	196.6	11.6	1201	4	US-09-016-434-1085
31	196.6	11.6	1201	4	US-09-023-655-905
32	196.6	11.6	1717	4	US-09-023-655-959
33	196.6	11.6	1915	3	US-08-575-967A-3
34	196.6	11.6	1915	4	US-08-771-276-3
35	194	11.4	2440	3	US-08-724-984A-1
36	193.4	11.4	1068	4	US-09-826-509-474
37	193.4	11.4	1689	4	US-08-720-565-1
38	193.4	11.4	1689	4	US-09-931-381A-15
39	193.4	11.4	1689	4	US-08-375-199B-1
40	192.6	11.3	1116	4	US-08-720-565-5
41	192.6	11.2	1495	4	US-08-375-199B-5
42	189.8	11.2	1495	4	US-09-016-434-1190
43	189.8	11.2	1495	4	US-09-023-655-1021
44	189.8	11.2	2156	1	US-08-012-988A-1
45	189.8	11.2	2156	4	US-09-023-655-1247

ALIGNMENTS

RESULT 1
US-10-039-659A-11
; Sequence 11, Application US/10039659A
; Patent No. 6723520
; GENERAL INFORMATION:
; APPLICANT: Wang, Wei
; APPLICANT: Gish, Kurt C.
; APPLICANT: Schall, Thomas J.
; APPLICANT: Vicari, Alain P.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Antibodies that bind chemokine TECK
; FILE REFERENCE: DX0589K1B US
; CURRENT APPLICATION NUMBER: US/10/039, 659A
; CURRENT FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: US 08/887,977
; PRIOR FILING DATE: 1997-07-03
; PRIOR APPLICATION NUMBER: US 60/021,664
; PRIOR FILING DATE: 1996-07-05
; PRIOR APPLICATION NUMBER: US 60/028,329
; PRIOR FILING DATE: 1996-10-11
; PRIOR APPLICATION NUMBER: US 60/048,593
; PRIOR FILING DATE: 1997-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (49)..(1116)
; OTHER INFORMATION:
US-10-039-659A-11

Query Match 85.3%; Score 1448.2; DB 4; Length 1547;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1450; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 245 GGCAGTCTCAAGATGGCCAAATTACAGCTGGCACAGAGAGTGAATATGATGTCCTCATA 304
Db 73 GGCAGTCTCAAGATGGCCAAATTACAGCTGGCACAGAGAGTGAATATGATGTCCTCATA 132
QY 305 GAAGGTGAATCTGGAGAGCGATGAGCAGAGCAATGTGACAAGTATGACGCCAGGCACTC 364
Db 133 GAAGGTGAATCTGGAGAGCGATGAGCAGAGCAATGTGACAAGTATGACGCCAGGCACTC 192
QY 365 TCAGCCAGCTGGTGGCCATCATCTGCTCTGCTGTTTGTGATCGGTGCTCTGGACAAT 424
Db 193 TCAGCCAGCTGGTGGCCATCATCTGCTCTGCTGTTTGTGATCGGTGCTCTGGACAAT 252

QY 425 CTCCTGGTTGTCCTTATCTCTGTAATAAATAAAGGACTCAACGCGTGGAAATATCTAT 484
 Db 253 CTCCTGGTTGTCCTTATCTCTGTAATAAATAAAGGACTCAACGCGTGGAAATATCTAT 312
 QY 485 CTTCTAAACCTTGGCAGTTCTTAACCTTGTTGTTCTTCTTACCTGCCCTTCTGGGCTCAT 544
 Db 313 CTTCTAAACCTTGGCAGTTCTTAACCTTGTTGTTCTTCTTACCTGCCCTTCTGGGCTCAT 372
 QY 545 GCTGGGGGGATCCCATGTTGTAATAATCTCATGTGACTGTACTTCTGTGGGCCCTGTACAGT 604
 Db 373 GCTGGGGGGATCCCATGTTGTAATAATCTCATGTGACTGTACTTCTGTGGGCCCTGTACAGT 432
 QY 605 GAGACATTTTCAATTTGCTCTGACTGTGCAAGGTACTAGTCTTTTGCACAGGSC 664
 Db 433 GAGACATTTTCAATTTGCTCTGACTGTGCAAGGTACTAGTCTTTTGCACAGGSC 492
 QY 665 AACTTTTTCTCAGCCAGGAGGAGGTCCTCTGTGGCATCATTTACAAGTGTCTCTGGCATGG 724
 Db 493 AACTTTTTCTCAGCCAGGAGGAGGTCCTCTGTGGCATCATTTACAAGTGTCTCTGGCATGG 552
 QY 725 GTAACAGCATTTCTGGCCACTTTGCTCTGAATAACGTTGTTTATAAACCTCAGATGGAAGAC 784
 Db 553 GTAACAGCATTTCTGGCCACTTTGCTCTGAATAACGTTGTTTATAAACCTCAGATGGAAGAC 612
 QY 785 CAGAAATACAGTGTGCAATTTAGCAGACTCCCTTCTGCGAGTGTAGAGACATTTCTGG 844
 Db 613 CAGAAATACAGTGTGCAATTTAGCAGACTCCCTTCTGCGAGTGTAGAGACATTTCTGG 672
 QY 845 AAGCATTTTCTGACCTTAAATAATGAACATTTCCGTTTCTTGTCTCTCCCTCATTTATTTT 904
 Db 673 AAGCATTTTCTGACCTTAAATAATGAACATTTCCGTTTCTTGTCTCTCCCTCATTTATTTT 732
 QY 905 ACATTTCTCTATGTGCAATGAAATAACATAAGTTTCAGGAGCAGAGTATAGCCTT 964
 Db 733 ACATTTCTCTATGTGCAATGAAATAACATAAGTTTCAGGAGCAGAGTATAGCCTT 792
 QY 965 TTCAGCTTGTTTTGGCCATATGTTAGTCTTCTCTGATGTGGGCCCTTACATATT 1024
 Db 793 TTCAGCTTGTTTTGGCCATATGTTAGTCTTCTCTGATGTGGGCCCTTACATATT 852
 QY 1025 GCATTTTCTCTGCTCACTTTCAAGAAACACTTCTCCTGAGTGACTGCAAGAGCAGTAC 1084
 Db 853 GCATTTTCTCTGCTCACTTTCAAGAAACACTTCTCCTGAGTGACTGCAAGAGCAGTAC 912
 QY 1085 AATCTGGAACAAAGTGTTCATCATCAATAAATCATCGCCACCAACCATGCTGCTGATCAAC 1144
 Db 913 AATCTGGAACAAAGTGTTCATCATCAATAAATCATCGCCACCAACCATGCTGCTGATCAAC 972
 QY 1145 CCTCTCCTGTATGCGTTTCTGATGGGACATTTAGCAATACCTCTGCGCTGTTTCCAT 1204
 Db 973 CCTCTCCTGTATGCGTTTCTGATGGGACATTTAGCAATACCTCTGCGCTGTTTCCAT 1032
 QY 1205 CTGCGTAGTAACACCCACTTCAACCCAGGGGAGTCTGCAACAGGCACATCGAGGGA 1264
 Db 1033 CTGCGTAGTAACACCCACTTCAACCCAGGGGAGTCTGCAACAGGCACATCGAGGGA 1092
 QY 1265 GAACCTGACCATTTCCACCGAAGTGTAACTAGCATCCACAAATGCAAGAAATAACA 1324
 Db 1093 GAACCTGACCATTTCCACCGAAGTGTAACTAGCATCCACAAATGCAAGAAATAACA 1152
 QY 1325 TGGATTTTCTCTGCTGATTTATTTTCATGTAATTTTCTACACATTTGTATACAAATC 1384
 Db 1153 TGGATTTTCTCTGCTGATTTATTTTCATGTAATTTTCTACACATTTGTATACAAATC 1212
 QY 1385 GGATACAGGAAGAAAGGAGAGTGTAGCTTAACATTTGCTAAGCACTGAATTTGTCTCAG 1444
 Db 1213 GGATACAGGAAGAAAGGAGAGTGTAGCTTAACATTTGCTAAGCACTGAATTTGTCTCAG 1272
 QY 1445 GCAACCTGCAAGGCTCTTTTACAAACGTGAGCTCTTTCGCTCTTACCACCTTGTCCATAGT 1504
 Db 1273 GCAACCTGCAAGGCTCTTTTACAAACGTGAGCTCTTTCGCTCTTACCACCTTGTCCATAGT 1332
 QY 1505 GTGGATAGGACTAGTCTCATTTCTCTGAGAAGAAACTAAGCGCGGGAATTTGTCTTAG 1564

Db 1333 GTGGATAGGACTAGTCTCATTTCTCTGAGAAGAAACTAAGCGCGGAAATTTGTCTAAG 1392
 QY 1565 ATCACTTAACATAGGAAGTGGCAGAACTGATTTCTCAGCCCTGGTAGCATTTTCTCAGAGC 1624
 Db 1393 ATCACTTAACATAGGAAGTGGCAGAACTGATTTCTCAGCCCTGGTAGCATTTTCTCAGAGC 1452
 QY 1625 CTAGCCTTGGTCCAGAACATCAAACTCCAAACCTTGGGGAACAAACGACATGAATAAATG 1684
 Db 1453 CTAGCCTTGGTCCAGAACATCAAACTCCAAACCTTGGGGAACAAACGACATGAATAAATG 1512
 QY 1685 TATTTTAAACAT 1697
 Db 1513 TATTTTAAACAT 1525

RESULT 2
 US-09-016-434-756
 ; Sequence 756, Application US/09016434
 ; Patent No. 6500938
 ; GENERAL INFORMATION:
 ; APPLICANT: Janice Au-Young
 ; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
 ; NUMBER OF SEQUENCES: 1490
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: HEREWITH
 ; CLASSIFICATION:
 ; PRIOR APPLICATION NUMBER:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zeller, Karen J.
 ; REGISTRATION NUMBER: 37,071
 ; REFERENCE/DOCKET NUMBER: PA-0002 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 756:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1270 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: MPHNOT03
 ; CLONE: 442279
 ; US-09-016-434-756

Query Match 74.7%; Score 1268; DB 4; Length 1270;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1268; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 78 TGGGCGGGGTAGAGCCACAGGGGAATCAACAGTGTGTTCTCTGTCCTCCCTCAGGGTCAGG 137
 Db 1 TGGGCGGGGTAGAGCCACAGGGGAATCAACAGTGTGTTCTCTGTCCTCCCTCAGGGTCAGG 60
 QY 138 AGCAGTCTGATCAAAAGGAGGCGCATCCACTGTGCGGGGCAATTCACACAGCTCCCGGATG 197

QY 366 CAGCCAGCTGGTGCACCTCACTCTGCTCTGCTGTGTTGTGATCGGTGCTCGCAATC 425
DB 185 CAGCCAGCTGGTGCACCTCACTCTGCTCTGCTGTGTTGTGATCGGTGCTCGCAATC 244
QY 426 TCTGTGTTGCTTATCTCTGTTAAATATAAAGGACTCAACGCGTGGAAATATCTATC 485
DB 245 TCTGTGTTGCTTATCTCTGTTAAATATAAAGGACTCAACGCGTGGAAATATCTATC 304
QY 486 TTCTAAACTTGGCAGTTTCTAACTGTGTTCTTCTGCTTACCCTGCCCTTCTGGCTCATG 545
DB 305 TTCTAAACTTGGCAGTTTCTAACTGTGTTCTTCTGCTTACCCTGCCCTTCTGGCTCATG 364
QY 546 CTGGGGGCATCCCATGTGTAAATTTCTATTGGACTGTCTGCGGCTGTACAGTG 605
DB 365 CTGGGGGCATCCCATGTGTAAATTTCTATTGGACTGTCTGCGGCTGTACAGTG 424
QY 606 AGACATTTTCAATTGCTTCTGACTGTGCAAGGTACCTAGTGTGTTTGGCAAGGGCA 665
DB 425 AGACATTTTCAATTGCTTCTGACTGTGCAAGGTACCTAGTGTGTTTGGCAAGGGCA 484
QY 666 ACTTTTCTCAGCAGGAGGGTCCCTGTGGCAATTAACAAGTGTCTGGCATGG 725
DB 485 ACTTTTCTCAGCAGGAGGGTCCCTGTGGCAATTAACAAGTGTCTGGCATGG 544
QY 726 TACAGCCATTCTGGCCACTTTCCTGTAATAGTGTGTTTATAAAGTGTGGAAGACC 785
DB 545 TACAGCCATTCTGGCCACTTTCCTGTAATAGTGTGTTTATAAAGTGTGGAAGACC 604
QY 786 AGAATAACAAGTGTGATTTAGCAGAACTTCTGCTGCGAGCTGATGAGACATCTGA 845
DB 605 AGAATAACAAGTGTGATTTAGCAGAACTTCTGCTGCGAGCTGATGAGACATCTGA 664
QY 846 AGCATTTTCTGACTTTTAAATAAGACATTTTGGTCTTGTCTCCCTTATTTATTTTA 905
DB 665 AGCATTTTCTGACTTTTAAATAAGACATTTTGGTCTTGTCTCCCTTATTTATTTTA 724
QY 906 CATTTCTCTATGCAATAGCAAAACACTAAGTTTCAAGGAGCAGAGTATAGCCTTT 965
DB 725 CATTTCTCTATGCAATAGCAAAACACTAAGTTTCAAGGAGCAGAGTATAGCCTTT 784
QY 966 TCAAGCTGTGTTTGGCAATAGTGTCTTCTGATGTTGGGCGCCCTACATATTG 1025
DB 785 TCAAGCTGTGTTTGGCAATAGTGTCTTCTGATGTTGGGCGCCCTACATATTG 844
QY 1026 CATTTTCTGCTCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTACA 1085
DB 845 CATTTTCTGCTCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTACA 904
QY 1086 ATCTGGACAAAAGTGTTCATCATCACTAAACTATGCGCCACCCCACTGCTGCATCAACC 1145
DB 905 ATCTGGACAAAAGTGTTCATCATCACTAAACTATGCGCCACCCCACTGCTGCATCAACC 964
QY 1146 CTCTCTGTATGGTTTCTTGTATGGGACATTTAGCAAAATACCTCTGCGGCTGTTTCCATC 1205
DB 965 CTCTCTGTATGGTTTCTTGTATGGGACATTTAGCAAAATACCTCTGCGGCTGTTTCCATC 1024
QY 1206 TCGGTAGTAACCCCACTTCAACCC 1231
DB 1025 TCGGTAGTAACCCCACTTCAACCC 1050

RESULT 4

US-09-023-655-308
; Sequence 308, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; EXPRESSION
; NUMBER OF SEQUENCES: 1508

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 308:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 620 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGN0T10
; CLONE: 1378524
; US-09-023-655-308

Query Match 35.2%; Score 597.8; DB 4; Length 620;
Best Local Similarity 99.2%; Pred. No. 1.le-179;
Matches 610; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 964 TTTCAAGCTGTGTTTGGCATAATGGTAGTCTTCTCTCTGATGTGGCGCCCTACAATAT 1023
DB 5 TTTCAAGCTGTGTTTGGCATAATGGTAGTCTTCTCTCTGATGTGGCGCCCTACAATAT 64
QY 1024 TGCATTTTCTGTCTCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTA 1083
DB 65 TGCATTTTCTGTCTCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTA 124
QY 1084 CAATCTGGACAAAAGTGTTCATCATCACTAAACTCATGCCACCACCCCACTGCTGCATCAA 1143
DB 125 CAATCTGGACAAAAGTGTTCATCATCACTAAACTCATGCCACCACCCCACTGCTGCATCAA 184
QY 1144 CCCTCTCTGTATGTTTCTTGTATGGGACATTTAGCAAAATACCTCTCCCGTGTGTTTCCA 1203
DB 185 CCCTCTCTGTATGTTTCTTGTATGGGACATTTAGCAAAATACCTCTGCGGCTGTGTTTCCA 244
QY 1204 TCTGCTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCAAGGACATCGAGGGA 1263
DB 245 TCTGCTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCAAGGACATCGAGGGA 304
QY 1264 AGACCTGACCATTTCCACCAGAGTGTAAACTAGCATCCACCMAATGCAAGAGAAATAAAC 1323
DB 305 AGACCTGACCATTTCCACCAGAGTGTAAACTAGCATCCACCMAATGCAAGAGAAATAAAC 364
QY 1324 ATGGAATTTTCTTCTGTGCAATTTTCTCATGTAAATTTTCTACACATTTGTATACAAAT 1383
DB 365 ATGGAATTTTCTTCTGTGCAATTTTCTCATGTAAATTTTCTACACATTTGTATACAAAT 424
QY 1384 CGGATACAGGAAGAAAGGAGAGTGAGCTAAACATTTGCTAAGCACTGAATTTGCTCTCA 1443
DB 425 CGGATACAGGAAGAAAGGAGAGTGAGCTAAACATTTGCTAAGCACTGAATTTGCTCTCA 484

Db 410 TAAAGCC---AGGACGGTCACCTTTGGGGTGGTGAAGTGTGATCACTTGGGTGGTGG 466
QY 732 CCATTCCTGGCCACTTCCCTGGAATACGTGGTTTATTAACCTCTCAGATGGAAGACCAAGAAAT 791
Db 467 CTGTGTTGGTCTCTCCAGGAATCATCTTTACAGATCTCAAAAGAAAGGTCTTCAT 526
QY 792 ACAAGTGTGATTTAGCAGAACTCCCTTCTGCGCAGCTGATGACATTTCTGGAAGCAAT 851
Db 527 ACACCT-----GCAGCTCTCATTTTCCATACAGTCAATCAATTTCTGGAAGAAAT 577
QY 852 TTCTGACTTTAAAAATGAACATTTGCTTCTTGTCTCCCTCCCTATTTATTTTACATTTTC 911
Db 578 TCAGACATTAAGATAGTATCATCTTGGGGTGGTCTGCGGCTGCTTGTGATGCTCATCT 637
QY 912 TCTATGTGCAAAATGAGAAAAACACTA-----AGTTTCAGGAGCAGAGGTATAGCC 962
Db 638 GCTACTCGGAATCTTAAAACTCTGCTCGGTGTCGAAATGAGAAGAGGACAGGG 697
QY 963 TTTTCAAGCTTGTGTTTGGCAATATGATGCTTCTTCTGATGTGGGCGCCCTACAATA 1022
Db 698 CTGTGAGGCTTATCTTCCACCATCATGATGTTTATTTCTTCTGCGGCTCCCTACAACA 757
QY 1023 TTGATATTTCTGTGTCACATTTCAAGAACATTTCTCCCTGAGTGAAGTCAAGAGCACT 1082
Db 758 TTGTCTCTCTCTGAACACCTTCCAGGAATTTCTTGGCCTGAAATTAATTTGAGTAGCTCTA 817
QY 1083 ACAATCTGACAAAAAGTTTCAATCACTAACTCATCGCCACCACCACCTGCTGCATCA 1142
Db 818 ACAGTTGGACCAAGCTATGAGGTGACAGACTCTTGGGATGACGCACTGCTGCATCA 877
QY 1143 ACCCTCTCTGTATGCTTTCTTGTAGGGACATTTAGCAAAATACCTCTGCGGCTGTTTCC 1202
Db 878 ACCCATCATCTATGCTTTGTGGGAGAGTTCAGAACTACCTTGTAGTCTTCTTCTTCC 937
QY 1203 ATCTGCGTAGTAACA 1217
Db 938 AAAAGCACATTTGCCA 952

RESULT 8

US-09-023-655-967

Sequence 967, Application US/09023655

Patent No. 6607879

GENERAL INFORMATION:

APPLICANT: Cocks, Benjamin G.

APPLICANT: Susan G. Stuart

APPLICANT: Jeffrey J. Seilhamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

TITLE OF INVENTION: EXPRESSION

NUMBER OF SEQUENCES: 1508

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,655

FILING DATE: HERewith

CLASSIFICATION:

PRIOR APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0001 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 967:

SEQUENCE CHARACTERISTICS:

LENGTH: 1225 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: g1502408

US-09-023-655-967

Query Match 13.6%; Score 230.6; DB 4; Length 1225;

Best Local Similarity 57.0%; Pred. No. 2.1e-82;

Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;

QY 330 CAGAGCAATGTGACAAAGTATGACGCCCAGGCACCTCTCAGGCCAGCTGGTGCCATCACTCT 389

Db 76 CGGAGCCCTGCCAAAATAATCAATGTGAAGCAATCGGAGCCCGCTCTCGCTCCGCTCT 135

QY 390 GCTCTGCTGTGTTGTGATCGGTGCTCTGACAAATCTCCTGGTGTGCTTATCTCTGATAA 449

Db 136 ACTCACTGGTGTTCATCTTTGTTGTTGGCAACATGCTGGTCACTCTCATCTCTGATAA 195

QY 450 AATATAAGAGCTCAAAACGGTGGAAATATCTATCTTAACTTGGGAGTTCCTAACT 509

Db 196 ACTGCAAAAGGCTGAAGAGCATGACATCTACCTGCTCAACCTGGCCATCTCTGACC 255

QY 510 TGTGTTTCTTGTCTTACCTTCTGCGCTCATGCTGGGGCG-----554

Db 256 TGTGTTTCTTGTCTTACCTTCTGCGCTCATGCTGGGGCG-----554

QY 555 ---ATCCCATGTGTAATAATTTCTCATTTGGAATGCTGCTGGGGCG-----554

Db 316 GAAATACAAATGTGCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCT 375

QY 612 TTTTCAATTTGCTTCTGACTGTGCAAAAGTACTAGTGTGTTTGGCAAGGGCAACTTTT 671

Db 376 TCTTCATCATCTCTCTGACAAATCGATAGGTACCTGGCTGTGCTGCTGCTGCTGCTT 435

QY 672 TCTCAGCAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 731

Db 436 TAAAGCC---AGGACGGTCACTTTGGGGTGGTGAAGTGTGATGATGATGATGATGATG 492

QY 732 CCATTTCTGCGCACCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 791

Db 493 CTGTGTTGCGTCTCTCCAGGAATCATCTTTACAGATCTCAAAAAGAGGTCTTCTCAT 552

QY 792 ACAGTGTGATTTAGCAGAACTCCCTTCTGCGCAGCTGATGAGACATTTCTGAGAGCAT 851

Db 553 ACACCT-----GCAGCTCTCATTTTCCATACAGTCAATCAATTTCTGGAAGAAAT 603

QY 852 TTCTGACTTTTAAAAATGAACATTTTCTGCTCTCCCTCTATTTTATTTTATTTTACATTT 911

Db 604 TCAGACATTAAGATAGTATCTTTGGGGTGGTCTGCTGCGGCTGTGCTGCTGCTGCTGCT 663

QY 912 TCTATGTGCAAAATGAGAAAAACACTA-----AGTTTCAGGAGCAGAGGTATAGCC 962

Db 664 GCTACTCGGAATCTTAAAACTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723

QY 963 TTTTCAAGCTTGTGTTTGGCAATATGATGCTTCTCTGATGTTGGGGCCCTACAATA 1022

Db 724 CTGTGAGGCTTATCTTCAACCATCATGATTTTATTTTCTTCTGCGGCTCCCTACAACA 783

QY 1023 TTGCAATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1082

Db 784 TTGCTCTTCTGAAACACTTCCAGGAATTTCTTGGCCTGAAATATTTGAGTAGTCTCTA 843

QY 1083 ACAATCTGCAAAAAGTGTTCATCACTCACTAAACTCATCGCCACCACCTGCTGCTGCTCA 1142

Db 844 ACAGTTGACCAAGCTATGCGAGTGCACAGACTCTTGGGATGACGCACTGCTGCATCA 903
QY 1143 ACCCTCTCTGTATGCTTCTTGATGGACATTTAGCAAAATACCTCTGCCGCTGTTCC 1202
Db 904 ACCCATCATCTATGCTTGTGCGGGAAGTTGAGAAATACCTCTTGTAGTCTTCTTCC 963
QY 1203 ATCTGCGTAGTAACA 1217
Db 964 AAAAGCACATTGCCA 978

RESULT 9
US-09-087-232A-12
; Sequence 12, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1376 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 240..1298
US-09-087-232A-12

Query Match 13.6%; Score 230.6; DB 3; Length 1376;
Best Local Similarity 57.0%; Pred. No. 2.2e-62;
Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;
QY 330 CAGAGCAATGTGACAGTATGACGCCGCACTCTCAGCCGAGCTGTGGCATCACTCT 389
Db 289 CGGAGCCCTGCCAAAAATCAATGTGAACAAATCGAGCCGCTCCTGCTCGCTCT 348
QY 390 GCTCTGCTGTTGTGATCGGTGTCCTGGAACAATCTCTGTTGTGCTTATCTCGTAA 449
Db 349 ACTCACTGTTGTATCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 408
QY 450 AATATAAGGACTCAACCGCTGGAAATATCTATCTTCTTAACCTTGGCAGTTCTTA 509

Db 409 ACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACC 468
QY 510 TGTGTTTCTTGGTTTACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 554
Db 469 TGTGTTTCTTGGTTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 528
QY 555 ---ATCCCATCTGTAATAATTTCTCATTTGACATGTAATCTGCTGCTGCTGCTGCTGCTGCT 611
Db 529 GAAATACAAATGTCACACTCTTTGACAGGGCTCTATTTTATAGGCTCTTCTCTCGAAATCT 588
QY 612 TTTTCAATTTGCTTCTGACTGTGCAAAAGGTACCTAGTGTGTTTGTGCAAGGGCAACTTTT 671
Db 589 TCTTCATCATCTCTCTGACAAATGATAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 648
QY 672 TCTCAGCCAGGAGGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 731
Db 649 TAAAGGCC---AGGACGGTCACTTTGGGGTGGTGACAAAGTGTGATCACTCTTGGTGGTGG 705
QY 732 CCATTTCTGGCCACTTTGCTGCTGAATACGTTGTTTATAAACCTCAGATGGAAGACCAAGAT 791
Db 706 CTGTGTTTGGCTCTCTCCAGGAATCATCTTTACAGATCTCAAAAAGAGGTCTTCAAT 765
QY 792 ACAAGTGTGCATTTAGCAGAACTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 851
Db 766 ACACCT-----GCAGCTCTCATTTTCCATACAGTCAGTATCAATTTCTGGAAGAT 816
QY 852 TTCTGACTTTTAAATAAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 911
Db 817 TCCAGACATTAAGATAGTATCTTGGGGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 876
QY 912 TCTATGTGCAATGAGAAACACTA-----AGGTTCAGGAGGAGGAGGTATAGCC 962
Db 877 GCTACTCGGGAATCCTAAAAAATCTGCTTCCGCTGCGAAATGAGAAAGAGGACACAGG 936
QY 963 TTTTCAAGCTTTGTTTGGCCATAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1022
Db 937 CTGTGAGCTTATCTTCAACATCATGATGTTTATTTCTTCTTGGGCTCCCTACACA 996
QY 1023 TTGCAATTTTCTGCTGCTGCTTCAAGAACTTCTCCTGAGTGACTGCGAAGAGCAGCT 1082
Db 997 TTGCTCTTCTCTGAAACACCTTCCAGGAATTTCTTGGCTGCAATAATTTGCAAGTAGCT 1056
QY 1083 ACAATCTGGACAAAGTGTTCACATCACTAACTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1142
Db 1057 ACAGTTGGACCAAGCTATGCGAGTGCAGAGACTTTGGGATGACGCACTGCTGCATCA 1116
QY 1143 ACCCTCTCTGATGCTGCTTCTGATGGGCAATTTAGCAAAATACCTCTGCTGCTGCTGCT 1202
Db 1117 ACCCATCATCTATGCTTCTGCTGCGGGAAGTTTCAAGAACTACCTCTTAGTCTTCTTCC 1176
QY 1203 ATCTGCGTAGTAACA 1217
Db 1177 AAAAGCACATTGCCA 1191

RESULT 10
US-09-016-434-1104
; Sequence 1104, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1376 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: G1262810
; US-09-016-434-1104

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Query Match      13.6%; Score 230.6; DB 4; Length 1376;
Best Local Similarity 57.0%; Pred. No. 2.2e-62;
Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;

QY 330 CAGAGCAATGTGACAGTATGAGCCGAGGACCTCTCAGCCAGCTGGTGCCATCACTCT 389
DB 289 CGGAGCCCTGCCAAAATAATCAATGTGAAGCAAAATCGACGCCGCTCTCGCTCCGCTCT 348
QY 390 GCTCTGCTGTGTGTGATCGGTGCTCGGACAAATCTCCTGTGTGTGTGCTTATCTGTAA 449
DB 349 ACTCACTGTGTGTATCTTTGGTTTGTGGCAACATGCTGGTCACTCTCATCTCATATA 408
QY 450 AATATAAGGACTCAACCGGTGGAAATATCTATCTTCTAACTTGGCAGTTTCTAACT 509
DB 409 ACTGCAAAAGGCTGAAGAGCATGACATCTACCTGTCAACCTGGCCATCTCTGACC 468
QY 510 TGTGTTTCTGTCTACCTGCTTCTGGGCTCATGCTGGGGCG----- 554
DB 469 TGTGTTTCTGTCTACCTGCTTCTGGGCTCATGCTGGGGCG----- 528
QY 555 ----ATCCCATGTGTAATAATCTCATTGGACTGTACTTCTGGGCTGTAGTGAGACAT 611
DB 529 GAAATACAAATGTCAACTCTTTGACAGGGCTCTATTTATAGGCTTCTTCTCTGGAATCT 588
QY 612 TTTTCAATTCCTCTGACTGTGCAAGGTAATCTATCTTCTAACTTGGCAGTTTCTAACT 509
DB 589 TCTTCATCATCTCTCGTCAATCGATGATGCTGGCTGTGGTCACTGTGTGTGCTT 648
QY 672 TCTCAGCCAGGAGGGTGGCTGTGGCATCATTAAGAGTGTCTGGCATGGTAAACAG 731
DB 649 TAAAGGCC---AGGACGGTCACTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGG 705
QY 732 CCATTCGTGGCACTTTGCTGATAGTGTGTTTATTAACCTCAGATGGAAGACCAAAAT 791
DB 706 CTGTGTTGGTCTCTCCAGGAATCATCTTTACAGATCTCAAAAGAGGTCCTTCTT 765
QY 792 ACAAGTGTGCAATTTAGCAGAACTCCCTTCTCGCCAGCTGATGAGCAATTTCTGGAAGCAAT 851
DB 766 ACACCT-----GCAGCTCTCAATTTCCATACAGTCAATCAATTTCTGGAAGAT 816
QY 852 TTTGATCTTTAAATGAAATTTGGTCTTGTCTCCCTCTATTTATTTTACATTTTC 911
DB 817 TCCAGACATTAAGATAGTCACTTTGGGGTGGTCTGCTGGCTGTGTGTGCTGTCT 876

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QY 912 TCTATGTGCAATGACAGAAAACACTA-----AGGTTTCAGGAGCAGAGGTATAGCC 962
DB 877 GCTACTCGGAATCTTAAAAACTCTGCTCGGTGTCGAAATGAGAAGAGGACAGGG 936
QY 963 TTTTCAAGCTGTTTGTGGCATAATGTAGTCTTCTCTTCTGTGTGGGCGCCCTTACAATA 1022
DB 937 CTGTGAGGCTTATCTTCCACCATCATGATTTTCTTTCTCTCTGCGCTCCCTTACAACA 996
QY 1023 TTGCATTTTCTGTCCTCACTTTCAAGAACACATTTCTCCCTGAGTGTGCAAGAGGAGCT 1082
DB 997 TTGTCTCTTCTCTGAACACCTTCCAGGAATCTTTGGCCCTGAAATAATTGAGTAGCTCTA 1056
QY 1083 ACAATCTGGACAAAAGTGTTCACATCACTAAACTCATGCGCACACCCACTGTGTCATCA 1142
DB 1057 ACAGTTTGGACCAAGCTATGCGAGTGCACAGAGACTCTTGGGATGACGCACTGTGTCATCA 1116
QY 1143 ACCCTCTCTGTATGCGTTTCTTGTATGGGACATTTAGCAAAATACCTTGTGCGGTGTTTCC 1202
DB 1117 ACCCATCATCTATGCTTTGTGGGAGAAATTCAGAAACTACCTCTTAGTCTTCTTCC 1176
QY 1203 ATCTGCGTAGTAACA 1217
DB 1177 AAAGCACATTTGCCA 1191

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RESULT 11
US-09-796-202-2
; Sequence 2, Application US/09796202
; Patent No. 6548636
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPM/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: human
US-09-796-202-2

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Query Match      13.6%; Score 230.6; DB 4; Length 1376;
Best Local Similarity 57.0%; Pred. No. 2.2e-62;
Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;

QY 330 CAGAGCAATGTGACAGTATGAGCCGAGGACCTCTCAGCCAGCTGGTGCCATCACTCT 389
DB 289 CGGAGCCCTGCCAAAATAATCAATGTGAAGCAAAATCGACGCCGCTCTCTGCTCCGCTCT 348
QY 390 GCTCTGCTGTGTGTGATCGGTGCTCGGACAAATCTCCTGTGTGTGTGCTTATCTGTAA 449
DB 349 ACTCACTGTGTGTATCTTTGGTTTGTGGCAACATGCTGGTCACTCTCATCTCATATA 408
QY 450 AATATAAGGACTCAACCGGTGGAAATATCTATCTTCTAACTTGGCAGTTTCTAACT 509
DB 409 ACTGCAAAAGGCTGAAGAGCATGACATCTACCTGTCAACCTGGCCATCTCTGACC 468
QY 510 TGTGTTTCTGTCTACCTGCTTCTGGGCTCATGCTGGGGCG----- 554
DB 469 TGTGTTTCTGTCTACCTGCTTCTGGGCTCATGCTGGGGCGAGTGGGACTTTG 528
QY 555 ----ATCCCATGTGTAATAATCTCATTGGACTGTACTTCTGGGCTGTAGTGAGACAT 611
DB 529 GAAATACAAATGTCAACTCTTTGACAGGGCTCTATTTATAGGCTTCTTCTCTGGAATCT 588
QY 612 TTTTCAATTCCTCTGACTGTGCAAGGTAATCTATCTTCTAACTTGGCAGTTTCTAACT 509
DB 589 TCTTCATCATCTCTCGTCAATCGATGATGCTGGCTGTGGTCACTGTGTGTGCTT 648

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QY 672 TCTCAGCAGGAGGAGGTCCTGTGGCATCATTAAGTGTCTTGGCATGGTAACAG 731
Db 649 TAAAGCC---AGGACGGTCACTTTGGGGTGGTACAGTGTATCACTTGGGTGG 705
QY 732 CCAATCTGGCCACTTTGGCTGAATACGTGGTTTATAAACCCTCAGATGGAAGACAGAAAT 791
Db 706 CTGTGTTTGGCTCTCTCCAGGAATCATCTTTACAGATCTCAAAAGAGGTCTTCAT 765
QY 792 ACAAGTGTGCAATTTAGCAAACTCCCTTCCGCCAGCTGATGAGACATTTCTGGAAGCAAT 851
Db 766 ACACCT-----GCAGCTCTCAATTTTCCATACAGTCAGTATCAATTTCTGGAAGAAAT 816
QY 852 TTCTGACTTTAAATGACATTCGGTCTTGTCTCTCCCTATTTATTTTACATTTT 911
Db 817 TCAGACATTAAGATAGTATCTTTGGGGTGGTCTCGCTGTGTGTCATGGTCACT 876
QY 912 TCTATGTCAAAATGAGAAAACACTA-----AGGTTACGGGAGCAGAGGTATAGCC 962
Db 877 GCTACTCGGAATCTTAAAACTCTGCTTCGGTGTGCGAATGAGAAGAGGACAGGG 936
QY 963 TTTTCAAGCTTTTGTGCAATAATGGTAGTCTTCTTCTGATGTGGGGCCCTACAATA 1022
Db 937 CTGTAGGCTTATCTTCAACCATCATGATGTTTATTTTCTCTCTGGGCTCCCTACAACA 996
QY 1023 TTGCATTTTCTGTGCTCACTTTCAAGACACTTCTCCCTGAGTGAAGTGCAGAGCAGCT 1082
Db 997 TTGTCTCTCTGCAACACTTCCAGGAATCTTTGGGCTGAATTAATGTCAGTAGCTCTA 1056
QY 1083 ACAATCTGGACAAAAGTGTTCATCATCACTAAACTCATGCCACCACTCTGTCATCA 1142
Db 1057 ACAGGTTGACCAAGCTATGCAAGTGCAGAGACTCTTTGGGATGAGCACTGTCTGATCA 1116
QY 1143 ACCCTCTCTGTATGCTTTCTTGTATGGACATTTAGCAAAATPACCTCTGCCGCTGTTCC 1202
Db 1117 ACCCATCATCTATGCTTTGTGGGGAGAGTTTCAAGAACTACCTCTTAGTCTTCTTCC 1176
QY 1203 ATCTGGTAGTAACA 1217
Db 1177 AAAAGCACATGGCCA 1191

RESULT 12
US-09-502-783A-1
; Sequence 1, Application US/09502783A
; Patent No. 6511826
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCR5)
; FILE REFERENCE: 1488.1150006
; CURRENT APPLICATION NUMBER: US/09/502,783A
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (259)..(1314)
US-09-502-783A-1

Query Match 13.6%; Score 230.6; DB 4; Length 1414;
Best Local Similarity 57.0%; Pred. No. 2.3e-62;
Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;

QY 330 CAGAGCAATGTGACAGTATGAGCCCGAGGCACTCTCAGCCCGAGCTGGTGCCATCACTCT 389
Db 308 CGGAGCCCTGCCAAAAAATCAATGTGAACAAATCGACGCCCGCTCTCTGCTCTCTCTCT 367
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QY 390 GCTCTGCTGTGTTGTGTATCGGTCTCGGACAACTCTCTGTTGTGCTTATCTCTGTTAA 449
Db 368 ACTCACTGTGTTCATCTTGTGTTTGTGGGCAACATGCTGGTCACTCTCATCTCTGATAA 427
QY 450 AATAAAGGAGCTCAACGCGTGGAAAAATATCTATCTTCTAAACCTTGGCAGTCTTCTAACT 509
Db 428 ACTGAAAGGCTGAAGAGATGACTGACATCTACTGCTCAACCTGGCCATCTCTGACC 487
QY 510 TGTGTTCTTCTTACCTGCTTCTGGGCTCATGCTGGGGCG----- 554
Db 488 TGTGTTCTTCTTACTGTCTCCCTCTCTGGGCTCACTATGCTGCCGCCAGTGGGACTTTG 547
QY 555 ---ATCCCATGTGTAATAATCTCATTTGACGTGTACTCTGTTGGGCTGTAGTGTGAGACAT 611
Db 548 GAAATACAAATGTGCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCT 607
QY 612 TTTTCAATTTGCTTCTGACTGTGCAAAAGTACTAGTGTGTTTTCACAAGGGCAACTTTT 671
Db 608 TCTTCATCATCTCTCTGCAATCGATAGTACTGCTGGCTGTGTCATGCTGTGTTGCTT 667
QY 672 TCTCAGCCAGGAGGAGGTGCCCTGTGGCATCATTTACAAGTGTCTGTCATGGTGAACAG 731
Db 668 TAAAGCC---AGGACGGTCACTTTGGGGTGGTGAAGTGTGATCACTTGGTGGTGG 724
QY 732 CCAATCTGGCCACTTTGCTGTAATACGTGGTGTATTAACCTCAGATGGAAGACCAAGAAAT 791
Db 725 CTGTGTTTGGCTCTCTCCAGGAATCATCTTTACAGATCTCAAAAGAGGTCTTTCAT 784
QY 792 ACAAGTGTGCATTTAGCAGAACTCTCCCTCTGCCAGCTGTAGTGTGAGACATTTCTGGAAGCAAT 851
Db 785 ACACCT-----GCAGCTCTCATTTTCATACAGTCAGTATCAATTTCTGGAAGAAAT 835
QY 852 TTCTGACTTTTAAATAAGCAATTTTCGGTCTTGTGCTCTCCCTATTTATTTTATCATTTTC 911
Db 836 TCCAGACATTAAGATAGTATCTTGGGGCTGGTCTCTGGCTGTGCTGTGTCATGGTCACT 895
QY 912 TCTATGTCAANTGAGAAAACACTA-----AGGTTACGGGAGCAGAGGTATAGCC 962
Db 896 GCTACTCGGGAATCTTAAAACTCTGCTTCGGTGTGGAATGAGAAGAGGACAGGG 955
QY 963 TTTTCAAGCTTGTGTTTTCGCATATAGTGTGCTTCTTCTGATGTGGGCGCTTACAATA 1022
Db 956 CTGTGAGGCTTATCTTCAACATCATGATGTTTATTTCTCTCTCTGGGCTCCCTACACA 1015
QY 1023 TTGCATTTTCTGTGCTCACTTTTCAAGAACACTTCTCCCTGAGTGAAGTGCAGAGCAGCT 1082
Db 1016 TTGCTCTTCTCTGAAACACTTCCAGGAATCTTTTGGGCTGGAATTAATTTGACAGTAGCTCTA 1075
QY 1083 ACATCTGGACAAAAGTGTTCACATCACTAAACTCATGCCACCACTGCTGTCATCA 1142
Db 1076 ACAGTTGGACCAAGCTATGCAAGGTGACAGAGACTCTTTGGGATGACGCACTCTGATCA 1135
QY 1143 ACCCTCTCTGTATGCTTCTTGTATGGGACATTTAGCAAAATPACCTCTGCCGCTGTTCC 1202
Db 1136 ACCCATCATCTATGCTTGTGCGGGAGAGTTTGTGCGGGAGAGTTTCAAGAACTACCTCTTAGTCTTCTTCC 1195
QY 1203 ATCTGGTAGTAACA 1217
Db 1196 AAAAGCACATGGCCA 1210
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RESULT 13
US-09-502-784A-1
; Sequence 1, Application US/09502784A
; Patent No. 6743594
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Methods of Screening Using Human G-Protein
; TITLE OF INVENTION: Chemokine Receptor HDGNR10 (CCR5)
; FILE REFERENCE: 1488.1150005
; CURRENT APPLICATION NUMBER: US/09/502,784A
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; CURRENT FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (259)..(1314)
; OTHER INFORMATION:
US-09-502-784A-1

Query Match 13.6%; Score 230.6; DB 4; Length 1414;
Best Local Similarity 57.0%; Pred. No. 2.3e-62;
Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;
QY 330 CAGAGCAATGTGACAAAGTATGAGCCCGAGGCACTCTCAGCCGAGCTGGTGCATCACTCT 389
DB 308 CGGAGCCCTGCCAAAAAATCAATGTGAAGCAATCGAGCCGCGCTCTCGCCTCCGCTCT 367
QY 390 GCTCTGCTGTGTTGTGATCGGTCTCGGACAAATCTCTGGTGTGCTTATCTGTGTAA 449
DB 368 ACTCACTGGTGTTCATCTTTGGTTTGTGGGCAACATGCTGGTCATCTCTGATAA 427
QY 450 AATATAAGGACTCAAAAGCGGTGAAATATCTATCTTTAAACTTGGCAGTTTCTAACT 509
DB 428 ACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACTGGCCATCTCTGACC 487
QY 510 TGTGTTTCTTGTACCTCCCTCTGGGCTCATGCTGGGGG-----554
DB 488 TGTGTTTCTTGTACCTCCCTCTGGGCTCATGCTGGGGG-----554
QY 555 ---ATCCCATGTGTAATAATCTCATTGGAGTGTACTTCTGGGCTGTACAGTGAGACAT 611
DB 548 GAATACATGTGTCACTCTTGACAGGGCTCTATTTTATAGGCTTCTCTGGATCT 607
QY 612 TTTTCAATTCCTTCTGACTGTGCAAAAGTACTAGTGTGTTTGTGCAAGGGCAACTTTT 671
DB 608 TCTTCATCATCTCTGACAAATCGATAGGTACCTGGCTGCTGCCATGCTGTGTTGCTT 667
QY 672 TCTCAGCAGGAGGAGGTGCGCTGTGGCATCTTACAGTGTCTGGCATGGGTAAACAG 731
DB 668 TAAAGCC---AGGACGGTCACTTTGGGGTGTGACAAAGTGTGATCACTTTGGGTGGTG 724
QY 732 CCATTCTGGGCACCTTTGGCCTGAATACGTTGTTTATATAACCTCAGATGGAAGACAGAAAT 791
DB 725 CTGTGTTGGGTCTCTCCAGGATCATCTTTACCAGATCTCAAAAGAGGTCTTCATT 784
QY 792 ACAAGTGTGCAATTTAGCAGAACTCCCTTCTGCGCAGCTGATGACATCTGGAAGCAAT 851
DB 785 ACACCT-----GCAGCTCTCATTTTCCATACAGTCAATCAATCTGGAAGAAAT 835
QY 852 TTTCTGACTTTTAAATGAATTCGTTTCTGCTTCTCCCTCCCTCTTTTATTTTACATTTC 911
DB 836 TCCAGACATTTAAAGATAGTCACTTTGGGGTGGTCTGCGGCTGCTTGTCTATGCTCATCT 895
QY 912 TCTATGTGCAATGAGAAAAACACTA-----AGGTTTCAGGAGCAGAGTATAGCC 962
DB 896 GCTACTCGGAATCCTTAAACCTCTGCTCGGTGTGCAATGAGAGAGGACAGGG 955
QY 963 TTTTCAAGCTGTTTGTGCAATAGTGTCTTCTGATGTGGGCGCCCTCAACA 1022
DB 956 CTGTGAGGCTTATCTTCAACCATCATGATGTTTATTTTCTCTCTGSGCTCCCTCAACA 1015
QY 1023 TTGCATTTTCTGTCACACTTCAAGAACACTTCTCCCTGAGTGACTGCAAGAGAGCT 1082
DB 1016 TTGCTCTTCTCCTGAACACCTTCAGGAATTTCTTTGGCCTGAATAATTTGAGTACTCTA 1075

QY 1083 ACAATCTGGACAAAAGTGTTCATCACTAAACTCATCGCCACCCACTGCTGTCATCA 1142
DB 1076 ACAGGTTGGACCAAGCTATGACAGTGCAGAGACTCTTGGATGACGCACTGCTGTCATCA 1135
QY 1143 ACCCTCTCCTGTATGGTTTCTTGTATGGGACATTTAGCAAAATACCTCTGGCGCTGTTTC 1202
DB 1136 ACCCCATCATCTATGCTTTTGTGCGGGAGAAAGTTTCAGAAACTACCTCTTATGCTTTCTTC 1195
QY 1203 ATCTGCGTGTATGAACA 1217
DB 1196 AAAAGCACATTTGCCA 1210

RESULT 14
US-09-339-912A-1
; Sequence 1, Application US/09339912A
; Patent No. 6735519
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/339,912A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (259)..(1314)
; OTHER INFORMATION: Description of Artificial Sequence: Genomic
US-09-339-912A-1

Query Match 13.6%; Score 230.6; DB 4; Length 1414;
Best Local Similarity 57.0%; Pred. No. 2.3e-62;
Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;
QY 330 CAGAGCAATGTGACAAAGTATGAGCCCGAGGCACTCTCAGCCGAGCTGGTGCATCACTCT 389
DB 308 CGGAGCCCTGCCAAAAAATCAATGTGAAGCAATCGAGCCGCGCTCTCGCCTCCGCTCT 367
QY 390 GCTCTGCTGTGTTGTGATCGGTGTCTGGACAAATCTCTGGTGTGCTTATCTGTGTAA 449
DB 368 ACTCACTGGTGTTCATCTTTGGTTTGTGGGCAACATGCTGGTCATCTCTGATAA 427
QY 450 AATATAAGGACTCAAAAGCGGTGAAATATCTATCTTTAAACTTGGCAGTTTCTAACT 509
DB 428 ACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACTGGCCATCTCTGACC 487
QY 510 TGTGTTTCTTGTACCTCCCTCTGGGCTCATGCTGGGGG-----554
DB 488 TGTGTTTCTTGTACCTCCCTCTGGGCTCATGCTGGGGG-----554
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QY 612 TTTTCAATTCCTTCTGACTGTGCAAAAGTACTAGTGTGTTTGTGCAAGGGCAACTTTT 671
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; Sequence 1, Application US/09195662A
; Patent No. 6800729
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGNR10 (CCR5 Receptor)
; FILE REFERENCE: 1488.1150002
; CURRENT APPLICATION NUMBER: US/09/195,662A
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (259)..(1314)
; OTHER INFORMATION: Description of Artificial Sequence: Genomic
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Query Match 13.6%; Score 230.6; DB 4; Length 1414;
Best Local Similarity 57.0%; Pred. No. 2.3e-62;
Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;
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QY 450 AATATAAGGACTCAACGCGTGGAAAATATCTATCTTTCTAAACTTGGCAGTTTCTTAAC 509
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Job time : 310 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 18, 2005, 15:44:41 ; Search time 1070 Seconds
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Title: AF014958

Perfect score: 1698

Sequence: 1 AGACGGTTCAGATCCCTCT.....TAAATGATATTTAAACATC 1698

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6054689 seqs, 3103772919 residues

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1693.6	99.7	1776	21	US-10-741-600-13
3	1468.4	86.5	1475	15	US-10-223-085-15
4	1468.4	86.5	1475	15	US-10-223-084-15
5	1468.4	86.5	1475	15	US-10-223-088-15
6	1468.4	86.5	1475	15	US-10-223-090-15
7	1468.4	86.5	1475	15	US-10-223-087-15
					Sequence 300, Appl
					Sequence 13, Appl
					Sequence 15, Appl
					Sequence 15, Appl
					Sequence 15, Appl
					Sequence 15, Appl
					Sequence 15, Appl

8	1468.4	86.5	1475	15	US-10-223-083-15	Sequence 15, Appl
9	1468.4	86.5	1475	15	US-10-223-089-15	Sequence 15, Appl
10	1468.4	86.5	1475	16	US-10-223-081-15	Sequence 15, Appl
11	1468.4	86.5	1475	16	US-10-223-082-15	Sequence 15, Appl
12	1468.4	86.5	1475	17	US-10-305-654-15	Sequence 15, Appl
13	1468.4	86.5	1475	18	US-10-081-056-15	Sequence 15, Appl
14	1468.4	86.5	1475	18	US-10-081-056-15	Sequence 15, Appl
15	1455.2	85.7	143068	9	US-09-967-768A-316	Sequence 353, App
16	1455.2	85.7	143068	9	US-09-967-768A-316	Sequence 316, App
17	1452.8	85.6	1646	21	US-10-843-641A-6461	Sequence 6461, App
18	1452.8	85.6	1646	21	US-10-741-600-12	Sequence 12, Appl
19	1448.2	85.3	1547	14	US-10-741-600-12	Sequence 17557, A
20	1448.2	85.3	1547	19	US-10-039-659-11	Sequence 11, Appl
21	1448.2	85.3	1547	21	US-10-754-071-11	Sequence 11, Appl
22	1268	74.7	1270	17	US-10-759-860-11	Sequence 756, App
23	1267.6	74.7	1316	15	US-10-305-720-756	Sequence 3, Appl
24	1161.4	68.4	1251	20	US-10-095-876A-3	Sequence 5, Appl
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26	1031.8	60.8	1035	18	US-10-029-386-22780	Sequence 22780, A
27	996	58.7	7644	15	US-10-623-472-31	Sequence 31, Appl
28	981.2	57.8	1050	9	US-10-311-455-858	Sequence 858, App
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30	597.8	35.2	620	18	US-10-311-455-857	Sequence 857, App
31	505.2	29.8	588	14	US-10-641-643-308	Sequence 308, App
32	441	26.0	480	10	US-10-052-283-88	Sequence 88, Appl
33	422	24.2	1083	18	US-09-918-995-22881	Sequence 22881, A
34	360.4	21.2	370	17	US-10-623-472-32	Sequence 32, Appl
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36	303.8	17.9	548	16	US-10-085-783A-20554	Sequence 20554, A
37	233	13.7	1059	13	US-10-029-386-9067	Sequence 9067, App
38	233	13.7	1059	14	US-10-106-623-19	Sequence 19, Appl
39	233	13.7	1059	20	US-10-151-274-8	Sequence 8, Appl
40	230.6	13.6	1056	9	US-10-772-037-19	Sequence 19, Appl
41	230.6	13.6	1056	9	US-09-779-879A-21	Sequence 21, Appl
42	230.6	13.6	1056	15	US-09-779-880A-21	Sequence 21, Appl
43	230.6	13.6	1056	16	US-10-067-800-21	Sequence 21, Appl
44	230.6	13.6	1059	15	US-10-135-839-21	Sequence 21, Appl
45	230.6	13.6	1225	9	US-10-290-058A-5	Sequence 5, Appl
					US-09-813-653-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-10-717-597-300
; Sequence 300, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dörner, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 300
; LENGTH: 1698
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-717-597-300

Query Match 100.0%; Score 1698; DB 19; Length 1698;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1698; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1681 AATGTATTTTAAACATC 1698
DB 1681 AATGTATTTTAAACATC 1698

RESULT 2

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; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; NUMBER OF SEQ ID NOS: 2003-12-22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Homo sapiens
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; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
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; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-223-085-15

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DB 241 CGTGAAATAATCTATCTTTCTAAACTTGGCAGTCTTAACTTGTGTTCTTCTTACCCT 300
QY 529 GCGCTCTGGCTCATGCTGGGGCGATCCCATGTGTAATAATCTCATTTGGACTGTACTT 588
DB 301 GCGCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAATAATCTCATTTGGACTGTACTT 360
QY 589 CGTGGSCCTGTACAGTGACACATTTTTCATTTGCCCTTCTGACTGTGCAAGGTACTAGT 648
DB 361 CGTGGSCCTGTACAGTGACACATTTTTCATTTGCCCTTCTGACTGTGCAAGGTACTAGT 420
QY 649 GTTTTGTGCAAGGGCAACTTTTCTCAGCCAGGAGGGTGCCTGTGGCATCATTTAC 708
DB 421 GTTTTGTGCAAGGGCAACTTTTCTCAGCCAGGAGGGTGCCTGTGGCATCATTTAC 480
QY 709 AAGTGTCTGGCATGGTAAAGCCATTTCTGGCCACTTTGCGCTGAATAGCTGGTTTATA 768
DB 481 AAGTGTCTGGCATGGTAAAGCCATTTCTGGCCACTTTGCGCTGAATAGCTGGTTTATA 540
QY 769 ACTCAGATGGAAGACCAAGAAATACAAAGTGTGCATTTAGCAGAACTCCCTTCTGCCAGC 828
DB 541 ACTCAGATGGAAGACCAAGAAATACAAAGTGTGCATTTAGCAGAACTCCCTTCTGCCAGC 600
QY 829 TGATGAGACATTTCTGGAAGCAATTTTCTGATCTTTTAAATAATGAACATTTCCGTTCTTGTCT 888
DB 601 TGATGAGACATTTCTGGAAGCAATTTTCTGATCTTTTAAATAATGAACATTTCCGTTCTTGTCT 660
QY 889 CCCCCATTTATTTTACATTTCTATGTGCAATAGAAAAACACTAAGTTTCAGGA 948
DB 661 CCCCCATTTATTTTACATTTCTATGTGCAATAGAAAAACACTAAGTTTCAGGA 720
QY 949 GCAGAGGTATAGCCTTTTCAGCTGTTTGTGTCATATGTTAGTCTTCTTCTGTATGTG 1008
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DB 721 GCAGAGGTATAGCCTTTTCAGCTGTTTGTGTCATATGTTAGTCTTCTTCTGTATGTG 780
QY 1009 GCGCCCTTACAATATTTGCAATTTTCTCTGTCACTTTTCAAGAACTTCTCTCTGAGTGA 1068
DB 781 GCGCCCTTACAATATTTGCAATTTTCTCTGTCACTTTTCAAGAACTTCTCTCTGAGTGA 840
QY 1069 CTGCAAGAGCAGCTACAAATCTGGACAAAAGTGTTCACATCACTAACTCATCGCCACCAC 1128
DB 841 CTGCAAGAGCAGCTACAAATCTGGACAAAAGTGTTCACATCACTAACTCATCGCCACCAC 900
QY 1129 CCACGTCTGCATCAACCCCTCTCTGTATGCGTTCCTGTATGGGACATTTAGCAAAATACCT 1188
DB 901 CCACGTCTGCATCAACCCCTCTCTGTATGCGTTCCTGTATGGGACATTTAGCAAAATACCT 960
QY 1189 CTGCGCTGTTTCCATCTGCGTAGTAAACACCCCACTTCAACCCAGGGGCGAGTCTGCACA 1248
DB 961 CTGCGCTGTTTCCATCTGCGTAGTAAACACCCCACTTCAACCCAGGGGCGAGTCTGCACA 1020
QY 1249 AGGCATCTCGAGGGAAGAACCTTGACCATTTCCACCGAAGTGTAAACTAGCATCCCAAT 1308
DB 1021 AGGCATCTCGAGGGAAGAACCTTGACCATTTCCACCGAAGTGTAAACTAGCATCCCAAT 1080
QY 1309 GCAAGAAGATAAATCAATGGAATTTTTCATCTTCTGCAATTTTCACTGTAATTTTCTACAC 1368
DB 1081 GCAAGAAGATAAATCAATGGAATTTTTCATCTTCTGCAATTTTCACTGTAATTTTCTACAC 1140
QY 1369 ATTTGTATACAAAATCGGATACAGAAAGGAGAGGTGAGCTAACTTTTGTCTAAGC 1428
DB 1141 ATTTGTATACAAAATCGGATACAGAAAGGAGAGGTGAGCTAACTTTTGTCTAAGC 1200
QY 1429 ACTGAAATTTGCTCAGGCAACCGTCAAGGCTTTTACAAAGTGAAGTCTTCTGCGCTCT 1488
DB 1201 ACTGAAATTTGCTCAGGCAACCGTCAAGGCTTTTACAAAGTGAAGTCTTCTGCGCTCT 1260
QY 1489 ACCACTTCTCCATAGTGTGGATAGGACTAGTCTCTCATTTCTCTGAGAAGAACTAAGCG 1548
DB 1261 ACCACTTCTCCATAGTGTGGATAGGACTAGTCTCTCATTTCTCTGAGAAGAACTAAGCG 1320
QY 1549 CGGAAATTTGCTTAAGATCACCTTAAGTAGGAGTGGGAGAACTGATTTCTCAGCCCTGCT 1608
DB 1321 CGGAAATTTGCTTAAGATCACCTTAAGTAGGAGTGGGAGAACTGATTTCTCAGCCCTGCT 1380
QY 1609 AGCATTTCTCAGAGCCCTACGCTTGTCCAGAACTCAAACTCCAAACCTGGGGACAAA 1668
DB 1381 AGCATTTCTCAGAGCCCTACGCTTGTCCAGAACTCAAACTCCAAACCTGGGGACAAA 1440
QY 1669 GCACATGAAATAAATGTTATTTTAAACATC 1698
DB 1441 GCACATGAAATAAATGTTATTTTAAACATC 1470
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RESULT 4

US-10-223-084-15

; Sequence 15, Application US/10223084

; Publication No. US20030105011A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Masters, Scot A.

; APPLICANT: Pan, James

; APPLICANT: Stephan, Jean-Philippe P.

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Ye, Weilan

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

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; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1CS
; CURRENT APPLICATION NUMBER: US/10/223,084
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-223-084-15

Query Match      86.5%; Score 1468.4; DB 15; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 229 GGAGCTCAGCCAGTGGCGAGTCTGAAGATGGCCAAATTACACGCTGGCACCAGAGGATGA 288
DB 1 GGAGCTCAGCCAGTGGCGAGTCTGAAGATGGCCAAATTACACGCTGGCACCAGAGGATGA 60

QY 289 ATATGATGCTCTATAGAGGTGAACCTGGAGAGCGATAGGCGAGAGCAATGTGACAAGTA 348
DB 61 ATATGATGCTCTATAGAGGTGAACCTGGAGAGCGATAGGCGAGAGCAATGTGACAAGTA 120

QY 349 TGACGCCAGCGACTCTCAGCCAGCTGGTGCCATCACTCTGCTCTGCTGTTTCTGAT 408
DB 121 TGACGCCAGCGACTCTCAGCCAGCTGGTGCCATCACTCTGCTCTGCTGTTTCTGAT 180

QY 409 CGGTGTCCTGGACAATCTCCTGGTTGTGCTTTATCTCTGGTAAATAATAAAGGACTCAACG 468
DB 181 CGGTGTCCTGGACAATCTCCTGGTTGTGCTTTATCTCTGGTAAATAATAAAGGACTCAACG 240

QY 469 CGTGGAATAATCTATCTCTAACTTGGCAGTTTCTAACTTGTTGTTTCTTGTTACCTT 528
DB 241 CGTGGAATAATCTATCTCTAACTTGGCAGTTTCTAACTTGTTGTTTCTTGTTACCTT 300

QY 529 GCCCTTCTGGCTCATGCTGGGGGCGATCCCATGTGTAATAATCTCATTTGGACTGTACTT 588
DB 301 GCCCTTCTGGCTCATGCTGGGGGCGATCCCATGTGTAATAATCTCATTTGGACTGTACTT 360

QY 589 CGTGGGCTGTACAGTGAGACATTTTTCATTGCCCTTCTGACTGTGCAAGGTTACCTAGT 648
DB 361 CGTGGGCTGTACAGTGAGACATTTTTCATTGCCCTTCTGACTGTGCAAGGTTACCTAGT 420

QY 649 GTTTTGTGCAAGGGCAACTTTTTCAGCCAGGAGGGTGCCCTGTGGCATCATTTAC 708
DB 421 GTTTTGTGCAAGGGCAACTTTTTCAGCCAGGAGGGTGCCCTGTGGCATCATTTAC 480

QY 709 AAGTGTCTGGCATGGGTAAACAGCCATTCTGGCCACTTTGCCCTGATAGTGGTTATAA 768
DB 481 AAGTGTCTGGCATGGGTAAACAGCCATTCTGGCCACTTTGCCCTGATAGTGGTTATAA 540

QY 769 ACCTCAGATGGAAGACCAAGAAATACAAGTGTGCATTTTAGCAGAACTCCCTTCTCTGCCAGC 828
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DB 541 ACCTCAGATGGAAGACCAGAAATACAAGTGTGCATTTAGCAGAACTCCCTTCTCTGCCAGC 600
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QY 949 GCAGAGTATAGCTTTTCAAGCTTGTGTTTGGCAATAAGTGTCTTCTCTCTGATGTG 1008
DB 721 GCAGAGTATAGCTTTTCAAGCTTGTGTTTGGCAATAAGTGTCTTCTCTCTGATGTG 780
QY 1009 GGGGCCCTACAAATATTTGCAATTTTCTGTGTCACCTTTCAAGAACACTTCTCCCTGAGTGA 1068
DB 781 GGGGCCCTACAAATATTTGCAATTTTCTGTGTCACCTTTCAAGAACACTTCTCCCTGAGTGA 840
QY 1069 CTGCAAGAGCAGCTACAATCTGGACAAAGTGTTCACATCAGTAAATCTCATCGCCACAC 1128
DB 841 CTGCAAGAGCAGCTACAATCTGGACAAAGTGTTCACATCAGTAAATCTCATCGCCACAC 900
QY 1129 CCACTGCTGCATCAACCCCTCTCCTGTATGCGTTTCTTGTATGGGACATTTAGCAAAATACCT 1188
DB 901 CCACTGCTGCATCAACCCCTCTCCTGTATGCGTTTCTTGTATGGGACATTTAGCAAAATACCT 960
QY 1189 CTGCGCTGTTTCCATCTGCGTAGTAACACCCACCTTCAACCCAGGGGGGAGTCTGACACA 1248
DB 961 CTGCGCTGTTTCCATCTGCGTAGTAACACCCACCTTCAACCCAGGGGGGAGTCTGACACA 1020
QY 1249 AGGCACATCGAGGGAAGAACCTTGACCATTTCCACCGAAGTGTAACTAGCATCCACCACAAAT 1308
DB 1021 AGGCACATCGAGGGAAGAACCTTGACCATTTCCACCGAAGTGTAACTAGCATCCACCACAAAT 1080
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QY 1369 ATTTGTATACAAATTCGGATACAGGAAGAAAGGAGAGAGTGAAGTAAATTTTGTCTAAGC 1428
DB 1141 ATTTGTATACAAATTCGGATACAGGAAGAAAGGAGAGAGTGAAGTAAATTTTGTCTAAGC 1200
QY 1429 ACTGAATTTGCTCTCAGGCACCGTGCAGAGGCTCTTTTACAAACGTCAGCTCTTCGCTCCT 1488
DB 1201 ACTGAATTTGCTCTCAGGCACCGTGCAGAGGCTCTTTTACAAACGTCAGCTCTTCGCTCCT 1260
QY 1489 ACCACTTGTCCATAGTGTGGATAGGACTAGTCTCATTTTCTGAGAAAGAAACTAAGGCG 1548
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DB 1321 CGGAAATTTGTCTAAGATCATTAACTAGGAAGTGGCAGAACTGATTCTCCAGCCCTGGT 1380
QY 1609 ASCATTTGCTCAGACCTACGCTTGGTCCAGAACATCAAACTCCAAACCTCGGGGCAAA 1668
DB 1381 ASCATTTGCTCAGACCTACGCTTGGTCCAGAACATCAAACTCCAAACCTCGGGGCAAA 1440
QY 1669 CGCATGAAATAAATGTATTTTAAACATC 1698
DB 1441 CGCATGAAATAAATGTATTTTAAACATC 1470
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RESULT 5
US-10-223-088-15
; Sequence 15, Application US/10223088
; Publication No. US20030105012A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
```

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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235PIC6
; CURRENT APPLICATION NUMBER: US 10/223,088
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-223-088-15

Query Match      86.5%; Score 1468.4; DB 15; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 229 GGAGCTCAGCCAGTGGGCGAGTCTGAAGATGGCCAAATTACACGCTGGCACCAGAGGATGA 288
DB 1 GGAGCTCAGCCAGTGGGCGAGTCTGAAGATGGCCAAATTACACGCTGGCACCAGAGGATGA 60
QY 289 ATATGATGTCTCATAGAGGTGAACCTGGAGAGCGATGAGGAGAGCAATGTGACAAGTA 348
DB 61 ATATGATGTCTCATAGAGGTGAACCTGGAGAGCGATGAGGAGAGCAATGTGACAAGTA 120
QY 349 TGACGCCACAGGACATCTCAGCCAGCTGTGTGCATCACTCTGCTCTGTGTGTGTGTGTAT 408
DB 121 TGACGCCACAGGACATCTCAGCCAGCTGTGTGCATCACTCTGCTCTGTGTGTGTGTAT 180
QY 409 CGGTGTCTGGACAATCTCCTGGTGTGCTTATCCTGGTAAATAATAAGGACTCAAAAG 468
DB 181 CGGTGTCTGGACAATCTCCTGGTGTGCTTATCCTGGTAAATAATAAGGACTCAAAAG 240
QY 469 CGTGGAAAATATCTATCTTCTAAACTTGGCAGTTCCTAACTTGTGTGTCTTCTTACCCT 528
DB 241 CGTGGAAAATATCTATCTTCTAAACTTGGCAGTTCCTAACTTGTGTGTCTTCTTACCCT 300
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DB 301 GCCCTTCTGGGCTCATGTCTGGGGGGGATCCCATGTGTGTAATAATCTCATTTGGAATGTT 360
QY 589 CGTGGGCTGTACAGTGAGACATTTTTCATTTGCCTTCTGACTGTGCAAGGTACTAGT 648

361 CGTGGGCTGTACAGTGAGACATTTTTCATTTGCCTTCTGACTGTGCAAGGTACTAGT 420
649 GTTTTGTGCAAGGGCAACTTTTCTCAGCCAGGAGGAGGTGCCCTGTGGCATATTAC 708
421 GTTTTGTGCAAGGGCAACTTTTCTCAGCCAGGAGGAGGTGCCCTGTGGCATATTAC 480
709 AAGTGTCTGCGATGGGTAAACAGCATTTCTGGCCACTTTTGCCTGTAATAGTGTGTTATAA 768
481 AAGTGTCTGCGATGGGTAAACAGCATTTCTGGCCACTTTTGCCTGTAATAGTGTGTTATAA 540
769 ACCTCAGATGGAAGACCAAGAAATCAAGTGTGCAATTTAGCAGAACTCCCTTCTCGCAGC 828
541 ACCTCAGATGGAAGACCAAGAAATCAAGTGTGCAATTTAGCAGAACTCCCTTCTCGCAGC 600
829 TGATGAGACATTTCTGGAAGACATTTTCTGACTTTTAAAAATGAACATTTTCGGTTCCT 888
601 TGATGAGACATTTCTGGAAGACATTTTCTGACTTTTAAAAATGAACATTTTCGGTTCCT 660
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661 CCCCTATTTATTTTACATTTCTCTATGTGCAATGAGAAAAACACATAAGTTCAGGA 720
949 GCAGAGTATAGCCTTTTCAAGCTTTGTTTGGCCATAATGGTAGTCTTCTCTCATGTG 1008
721 GCAGAGTATAGCCTTTTCAAGCTTTGTTTGGCCATAATGGTAGTCTTCTCTCATGTG 780
1009 GGCGCCCTACAAATATGCAATTTTCTGTCCACTTTTCAAGAAACACTTCTCCCTGAGTGA 1068
781 GGCGCCCTACAAATATGCAATTTTCTGTCCACTTTTCAAGAAACACTTCTCCCTGAGTGA 840
1069 CTGCAAGAGCAGCTACAAATCTGGACAAAGTGTTCACATCACTAACTCATGCGCCACC 1128
841 CTGCAAGAGCAGCTACAAATCTGGACAAAGTGTTCACATCACTAACTCATGCGCCACC 900
1129 CCATGCTGCAATCAACCTCTCTGTATGCGTTTCTGATGGGACATTTAGCAATACCT 1188
901 CCATGCTGCAATCAACCTCTCTGTATGCGTTTCTGATGGGACATTTAGCAATACCT 960
1189 CTGCGCTGTTTCCATCTGCGTAGTAAACACCCCACTTCAACCCAGGGGGAGTCTGCACA 1248
961 CTGCGCTGTTTCCATCTGCGTAGTAAACACCCCACTTCAACCCAGGGGGAGTCTGCACA 1020
1249 AGGCACATCGAGGAGAGAACTGACCATTCACCGAAGTGTAAACTAGCATCCCAAT 1308
1021 AGGCACATCGAGGAGAGAACTGACCATTCACCGAAGTGTAAACTAGCATCCCAAT 1080
1309 GCAAGAAATAAACAATGATTTTCTGCTTCTGCAATTTTCTGTAATTTTCTACAC 1368
1081 GCAAGAAATAAACAATGATTTTCTGCTTCTGCAATTTTCTGTAATTTTCTACAC 1140
1369 ATTTGTATACAAAATCGGATACAGAAAGAGGAGAGGTAGCTAACTTTGCTAAGC 1428
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1429 ACTGAAATTTGCTCAGGCACCGTGCAGGCTTTTACAAAGTGTGCTTCTCGCTCCT 1488
1201 ACTGAAATTTGCTCAGGCACCGTGCAGGCTTTTACAAAGTGTGCTTCTCGCTCCT 1260
1489 ACCACTTGTCCATAGTGTGGATAGGACTAGTCTCATTTTCTCTGAGAAGAAACTAAGGG 1548
1261 ACCACTTGTCCATAGTGTGGATAGGACTAGTCTCATTTTCTCTGAGAAGAAACTAAGGG 1320
1549 CGGAAATTTGCTTAAGATCACTTAATAGGAAGTGGCAGAACTGATTTCTCCAGCCCTGGT 1608
1321 CGGAAATTTGCTTAAGATCACTTAATAGGAAGTGGCAGAACTGATTTCTCCAGCCCTGGT 1380
1609 AGCATTTGCTCAGACCTACCGTTGGTCCAGAACTCAAACTCCAAACCCCTGGGACAAA 1668
1381 AGCATTTGCTCAGACCTACCGTTGGTCCAGAACTCAAACTCCAAACCCCTGGGACAAA 1440
1669 CGACATGAAATAAATGATTTTAAAAACATC 1698
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Db 1441 CGACATGAATAAATGATTATTTAAACATC 1470

RESULT 6

US-10-223-090-15

; Sequence 15, Application US/10223090

; Publication No. US20030105013A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Marsters, Scot A.

; APPLICANT: Pan, James

; APPLICANT: Stephan, Jean-Philippe F.

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Williams, P.Mickey

; APPLICANT: Ye, Weilan

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

; FILE REFERENCE: P3235P1C2

; CURRENT APPLICATION NUMBER: US/10/223,090

; CURRENT FILING DATE: 2002-08-16

; PRIOR APPLICATION NUMBER: US 10/081,056

; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: US 60/213,637

; PRIOR FILING DATE: 2000-06-23

; PRIOR APPLICATION NUMBER: US 60/219,556

; PRIOR FILING DATE: 2000-07-20

; PRIOR APPLICATION NUMBER: US 60/220,624

; PRIOR FILING DATE: 2000-07-25

; PRIOR APPLICATION NUMBER: US 60/220,664

; PRIOR FILING DATE: 2000-07-25

; PRIOR APPLICATION NUMBER: PCT/US00/20710

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: US 60/222,695

; PRIOR FILING DATE: 2000-08-02

; PRIOR APPLICATION NUMBER: US 09/643,657

; PRIOR FILING DATE: 2000-08-17

; PRIOR APPLICATION NUMBER: PCT/US00/23522

; PRIOR FILING DATE: 2000-08-23

; PRIOR APPLICATION NUMBER: PCT/US00/23328

; PRIOR FILING DATE: 2000-08-24

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 383

; SEQ ID NO 15

; LENGTH: 1475

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-223-090-15

Query Match 86.5%; Score 1468.4; DB 15; Length 1475;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 229 GGAGCTCAGCCAGTGGCAGTCTGAAGATGGCCAAATTACCGCTGGCACAGAGGATGA 288

Db 1 GGAGCTCAGCCAGTGGCAGTCTGAAGATGGCCAAATTACCGCTGGCACAGAGGATGA 60

QY 289 ATATGATGCTCATAGAAGGTGAATGGAGAGCGATAGGCGAGCAATGTGCAAGTA 348

Db 61 ATATGATGCTCATAGAAGGTGAATGGAGAGCGATAGGCGAGCAATGTGCAAGTA 120

QY 349 TGACGCCCGGCACTCTCAGCCAGCTGGTGCCATCACTCTGCTGCTGTTGTTGAT 408

Db 121 TGACGCCCGGCACTCTCAGCCAGCTGGTGCCATCACTCTGCTGCTGTTGTTGAT 180

QY 409 CGGTGTCCTGGACAAATCTCCTGTTGTTGTTTCTCTGTTAAATATAAAGGACTCAACG 468

181 CGGTGTCCTGGACAAATCTCCTGTTGTTGTTTCTCTGTTAAATATAAAGGACTCAACG 240

469 CGTGGAAATATCTATCTTCTAACTGGCAGTTTCTAACTTGTGTTCTTGTCTTACCCT 528

241 CGTGGAAATATCTATCTTCTAACTGGCAGTTTCTAACTTGTGTTCTTGTCTTACCCT 300

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601 TGATGAGACATTTCTGGAAGCATTTTCTGACTTTTAAATAAGAACTTTTGGTCTTGTGCT 660

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781 GGGCCCTACATATTTGCAATTTTCTGCTCCACTTTTCAAGAACACTTTCTCCCTGAGTGA 840

1069 CTGCAAGAGCAGCTACAAATCTGGACAAAAGTGTTCACATCACTAACTCATCGCCACCAC 1128

841 CTGCAAGAGCAGCTACAAATCTGGACAAAAGTGTTCACATCACTAACTCATCGCCACCAC 900

1129 CCACTGCTGCATCAACCCCTCTCTGATGCGTTTCTTGATGGACATTTAGCAAAATACCT 1188

901 CCACTGCTGCATCAACCCCTCTCTGATGCGTTTCTTGATGGACATTTAGCAAAATACCT 960

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961 CTGCGCTGTTTCCATCTCGGTAGTAACACCCCACTTTCAACCCAGGGGCGAGTCTGCACA 1020

1249 AGSCACATCGAGGAAGAACCTGACCATTTCCACCGAAGTGTAACTAGCATCCACCAAT 1308

1021 AGSCACATCGAGGAAGAACCTGACCATTTCCACCGAAGTGTAACTAGCATCCACCAAT 1080

1309 GCAAGAAGAAATAAATGGAATTTTCACTTTCTGCAATTTTCAATGTAATTTTCTACAC 1368

1081 GCAAGAAGAAATAAATGGAATTTTCACTTTCTGCAATTTTCAATGTAATTTTCTACAC 1140

1369 ATTTGTATCAAAATCGGATACAGGAGGAGGAGGAGTGTAGCTTAACTTGTCTAAGC 1428

1141 ATTTGTATCAAAATCGGATACAGGAGGAGGAGGAGTGTAGCTTAACTTGTCTAAGC 1200

1429 ACTGAATTTGCTCAGGACCGCTGCAAGGCTCTTTTCAAAAGCTGAGCTCTTCTGCTCTCT 1488

1201 ACTGAATTTGCTCAGGACCGCTGCAAGGCTCTTTTCAAAAGCTGAGCTCTTCTGCTCTCT 1260

1489 ACCACTGTGCTCAGTGTGGATAGGACTGTCTTCTTCTGAGAGGAGGAGGAGGAGGAGG 1548

Db	1361	ACCACTTGTCATAGTGGGATAGGACTAGTCTCATTTCTCTGAGAGAGAAAACCTAAGCGC	1320
Qy	1549	CGGAAATTTGTCTAAAGATCACTTAACTAGGAAGTGGCAGAACTGATTCTCCAGGCCCTGGT	1608
Db	1321	CGGAAATTTGTCTAAAGATCACTAATCACTAGGAGTGGCAGAACTGATTCTCCAGGCCCTGGT	1380
Qy	1609	AGCAATTTGCTCAGAGCCCTAGCGTTGGTCCAGAACATCAAACTCCAAACCCCTGGGGACAAA	1668
Db	1381	AGCAATTTGCTCAGAGCCCTAGCGTTGGTCCAGAACATCAAACTCCAAACCCCTGGGGACAAA	1440
Qy	1669	CGACATGAATAAATGTATTTTAAAAATC	1698
Db	1441	CGACATGAATAAATGTATTTTAAAAATC	1470

RESIN.T 7

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RES001 7
; Sequence 15, Application US/10223087
; Publication No. US20030109438A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austen L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235PIC4
; CURRENT APPLICATION NUMBER: US/10/223,087
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/230,978
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/232,887
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 09/664,610
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/242,922
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/709,238
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30952

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Qy 469 CGTGGAAATATCTATCTTCTAAACTTGGCAGTTTCTAACTTGTGTTTCTTGCTTACCCT 528
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Qy 529 GCCCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAAATTTCTCAITGGACTGTACTT 588
Db 301 GCCCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAAATTTCTCAITGGACTGTACTT 360
Qy 589 CGTGGGCTGTACAGTGAGACATTTTCAATTTGCTTCTGACTGTGCAAGGTACCTAGT 648
Db 361 CGTGGGCTGTACAGTGAGACATTTTCAATTTGCTTCTGACTGTGCAAGGTACCTAGT 420
Qy 649 GTTTTGTGCAAGGGCAACTTTTCTCAGCCAGAGGAGGTGCCCTGTGTGCATCATTTAC 708
Db 421 GTTTTGTGCAAGGGCAACTTTTCTCAGCCAGAGGAGGTGCCCTGTGTGCATCATTTAC 480
Qy 709 AAGTGTCTGCGCATGGGTACAGCCATTTCTGGCCACTTTGCGCTGAATACGTGTTTATA 768
Db 481 AAGTGTCTGCGCATGGGTACAGCCATTTCTGGCCACTTTGCGCTGAATACGTGTTTATA 540
Qy 769 ACCTCAGATGGAAGCAGACCAATTAACAAGTGTGCACTTTAGCAGAACTCCCTTCTGCCAGC 828
Db 541 ACCTCAGATGGAAGCAGACCAATTAACAAGTGTGCACTTTAGCAGAACTCCCTTCTGCCAGC 600
Qy 829 TGATGACATTTCTGGAAGCATTTTCTGACTTTTAAAAATGAACATTTTCGGTTCCTTGTCT 888
Db 601 TGATGACATTTCTGGAAGCATTTTCTGACTTTTAAAAATGAACATTTTCGGTTCCTTGTCT 660
Qy 889 CCCCCTATTATTTTACATTTCTATGTGCAATGCAAAATGAGAAAAACATTAAGTTTCAGGA 948
Db 661 CCCCCTATTATTTTACATTTCTATGTGCAATGCAAAATGAGAAAAACATTAAGTTTCAGGA 720
Qy 949 GCAGAGTATAGCTTTTCAAGCTGTTTGTGTCATATGCTAGTCTTCTCTGTATGTG 1008
Db 721 GCAGAGTATAGCTTTTCAAGCTGTTTGTGTCATATGCTAGTCTTCTCTGTATGTG 780
Qy 1009 GGGCCCTCAATATTTGCAATTTTCTGTCTCCACTTTTCAAGAAACATTTCTCCCTGAGTGA 1068
Db 781 GGGCCCTCAATATTTGCAATTTTCTGTCTCCACTTTTCAAGAAACATTTCTCCCTGAGTGA 840
Qy 1069 CTCGAAGCAGCTACATCTGACAAAGTGTTCATCATCACTAACTATCGCCACCAC 1128
Db 841 CTCGAAGCAGCTACATCTGACAAAGTGTTCATCATCACTAACTATCGCCACCAC 900
Qy 1129 CCACTGCTCATCAACCTCTCTGTATGCTTCTTGTGAGGACATTTAGCAAAATACCT 1188
Db 901 CCACTGCTCATCAACCTCTCTGTATGCTTCTTGTGAGGACATTTAGCAAAATACCT 960
Qy 1189 CTGCCGCTGTTTCCATCTGCTAGTAAACACCCCACTTTCAACCCAGGGGGCAGTCTGCACA 1248
Db 961 CTGCCGCTGTTTCCATCTGCTAGTAAACACCCCACTTTCAACCCAGGGGGCAGTCTGCACA 1020
Qy 1249 AGGCATCTCAGGGAAGAACTGACCAATTCACCGAAGTGTAACTAGCATCAACCAAT 1308
Db 1021 AGGCATCTCAGGGAAGAACTGACCAATTCACCGAAGTGTAACTAGCATCAACCAAT 1080
Qy 1309 GCAAGAAGATAAACAATGATTTTCTCTTCTGCAATTTTCTCATCTAAATTTTCTACAC 1368
Db 1081 GCAAGAAGATAAACAATGATTTTCTCTTCTGCAATTTTCTCATCTAAATTTTCTACAC 1140
Qy 1369 ATTTGTATACAAATCGGATACAGGAAGAAAGGAGAGGTGAGCTAAATTTGTCTAAGC 1428
Db 1141 ATTTGTATACAAATCGGATACAGGAAGAAAGGAGAGGTGAGCTAAATTTGTCTAAGC 1200
Qy 1429 ACTGAATTTGCTCAGCACCGTGCAGAGGTCTTTTACAAAGTGTCTCTTCCGCTCTCT 1488
Db 1201 ACTGAATTTGCTCAGCACCGTGCAGAGGTCTTTTACAAAGTGTCTCTTCCGCTCTCT 1260
Qy 1489 ACCACTTGTCCATAGTGTGATAGGACTAGTCTCATTTCTCTGAGAAGAAACATAAGGG 1548
Db 1261 ACCACTTGTCCATAGTGTGATAGGACTAGTCTCATTTCTCTGAGAAGAAACATAAGGG 1320

Qy 1549 CGGAAATTTGCTCTAAGATCACTTAACTAGGAAGTGGCAGAACTGATTTCTCCAGCCCTGGT 1608
Db 1321 CGGAAATTTGCTCTAAGATCACTAATACTAGGAAGTGGCAGAACTGATTTCTCCAGCCCTGGT 1380
Qy 1609 AGCATTTGCTCAGAGCCTACGCTTGTCTCAGAACTCAAACTCCAAACCCCTGGGGACAAA 1668
Db 1381 AGCATTTGCTCAGAGCCTACGCTTGTCTCAGAACTCAAACTCCAAACCCCTGGGGACAAA 1440
Qy 1669 CGACATGAAATAAATGATTTTAAACATC 1698
Db 1441 CGACATGAAATAAATGATTTTAAACATC 1470

RESULT 8

US-10-223-083-15
; Sequence 15, Application US/10223083
; Publication No. US20030119112A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scott A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235PIC8
; CURRENT APPLICATION NUMBER: US/10/223,083
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-223-083-15

Query Match 86.5%; Score 1468.4; DB 15; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 229 GGAGCTCAGCCCGAGTGGGCGAGTCTGAAGATGCCCAATTAACAGCTGGCACCAGAGATGA 288
Db 1 GGAGCTCAGCCCGAGTGGGCGAGTCTGAAGATGCCCAATTAACAGCTGGCACCAGAGATGA 60

QY 289 ATATGATGTCTCATAGAAAGGTGAACCTGGAGAGCGGATGAGGCGAGCAATGTGACAAGTA 348
DB 61 ATATGATGTCTCATAGAAAGGTGAACCTGGAGAGCGGATGAGGCGAGCAATGTGACAAGTA 120
QY 349 TGACGCCAGGCACTCTCAGCCAGCTGTGGCCACCTCTGCTCTGCTGTGTTGTGAT 408
DB 121 TGACGCCAGGCACTCTCAGCCAGCTGTGGCCACCTCTGCTCTGCTGTGTTGTGAT 180
QY 409 CGGTGTCCTGGCAATCTCTGCTGTGCTTATCTCTGGTAAATATAAAGGACTCAAAAG 468
DB 181 CGGTGTCCTGGCAATCTCTGCTGTGCTTATCTCTGGTAAATATAAAGGACTCAAAAG 240
QY 469 CGTGGAAATATCTATCTCTAAACCTGGGAGTTCTAACTGTGTTCTCTGCTTACCT 528
DB 241 CGTGGAAATATCTATCTCTAAACCTGGGAGTTCTAACTGTGTTCTCTGCTTACCT 300
QY 529 GCCCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAATAATCTCATTTGAGCTGTACT 588
DB 301 GCCCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAATAATCTCATTTGAGCTGTACT 360
QY 589 CGTGGCCCTGTACAGTGAGACATTTTTCATTTCAATTCCTGTGCTGCAAAAGGTACTAGT 648
DB 361 CGTGGCCCTGTACAGTGAGACATTTTTCATTTCAATTCCTGTGCTGCAAAAGGTACTAGT 420
QY 649 GTTTTGGCAAGGGCAACTTTTCTCAGCCAGGAGGGTGCCTGTGGCATCATTTAC 708
DB 421 GTTTTGGCAAGGGCAACTTTTCTCAGCCAGGAGGGTGCCTGTGGCATCATTTAC 480
QY 709 AGTGTCTGGGATGGTAAACAGCCATCTCGGCCACTTTTGCCTGAATACGTGTTTATAA 768
DB 481 AGTGTCTGGGATGGTAAACAGCCATCTCGGCCACTTTTGCCTGAATACGTGTTTATAA 540
QY 769 ACCTCAGATGGAAGACCAAGAAATACAAAGTGTGCTTTAGCAGAACTCCCTTCTGCCAGC 828
DB 541 ACCTCAGATGGAAGACCAAGAAATACAAAGTGTGCTTTAGCAGAACTCCCTTCTGCCAGC 600
QY 829 TGATGAGACATCTGGAAGCATTTTCTGACTTTTAAATGAACATTTGCTGTCT 888
DB 601 TGATGAGACATCTGGAAGCATTTTCTGACTTTTAAATGAACATTTGCTGTCT 660
QY 889 CCCCCTATTTATTTTACATTTCTATGTGCAATGAGAAACAACTAAGTTTCAGGA 948
DB 661 CCCCCTATTTATTTTACATTTCTATGTGCAATGAGAAACAACTAAGTTTCAGGA 720
QY 949 GCAGAGGTATAGCTTTTCAAGCTGTGTTTGGCATAATGGTAGTCTTCTCTGATGTG 1008
DB 721 GCAGAGGTATAGCTTTTCAAGCTGTGTTTGGCATAATGGTAGTCTTCTCTGATGTG 780
QY 1009 GGGGCCCTACATATTTGCAATTTTCTGTGCACTTTCAAGAACACTTCTCCCTGAGTGA 1068
DB 781 GGGGCCCTACATATTTGCAATTTTCTGTGCACTTTCAAGAACACTTCTCCCTGAGTGA 840
QY 1069 CTGCAAGAGCAGCTACAATCTGACAAAGTGTTCACATCACTAAACTCATGCCACAC 1128
DB 841 CTGCAAGAGCAGCTACAATCTGACAAAGTGTTCACATCACTAAACTCATGCCACAC 900
QY 1129 CCACTGCTGCATCAACCCCTCTCCTGTATGCGTTTCTTGATGGGACATTTAGCAAAATCCT 1188
DB 901 CCACTGCTGCATCAACCCCTCTCCTGTATGCGTTTCTTGATGGGACATTTAGCAAAATCCT 960
QY 1189 CTGCGCTGTTTCCATCTGCTAGTAAACCCCACTTGAACCCAGGGGCGAGTCTGCACA 1248
DB 961 CTGCGCTGTTTCCATCTGCTAGTAAACCCCACTTGAACCCAGGGGCGAGTCTGCACA 1020
QY 1249 AGGCACATCGAGGAAGAACCTGACCATTCACCCGAAGTGAACCTAGCATCCACCAAT 1308
DB 1021 AGGCACATCGAGGAAGAACCTGACCATTCACCCGAAGTGAACCTAGCATCCACCAAT 1080
QY 1309 GCAAGAAGATAAATGAGATTTTCACTTTCTGCAATATTTTCATGTAAATTTTCTACAC 1368
DB 1081 GCAAGAAGATAAATGAGATTTTCACTTTCTGCAATATTTTCTGCAATATTTTCTACAC 1140

RESULT 9

US-10-223-089-15
; Sequence 15, Application US/10223089
; Publication No. US20030125521A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235PLC9
; CURRENT APPLICATION NUMBER: US/10/223,089
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15


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; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-223-081-15

Query Match      86.5%; Score 1468.4; DB 16; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 229 GGAGCTCAGCCAGTGGGCGAGTCTGAAGATGGCCAAATTACACGCTGGCCACGAGGATGA 288
Db 1 GGAGCTCAGCCAGTGGGCGAGTCTGAAGATGGCCAAATTACACGCTGGCCACGAGGATGA 60
QY 289 ATATGATGTCTCATAGAGGTGAACCTGGAGAGCGATGAGGAGAGCAATGTGACAGTA 348
Db 61 ATATGATGTCTCATAGAGGTGAACCTGGAGAGCGATGAGGAGAGCAATGTGACAGTA 120
QY 349 TGACGCCAGGCACTCTCAGCCAGCTGGTGCCATCAGTCTGCTGCTGCTGTTGTGAT 408
Db 121 TGACGCCAGGCACTCTCAGCCAGCTGGTGCCATCAGTCTGCTGCTGCTGTTGTGAT 180
QY 409 CGGTGTCCTGGCAATCTCTCTGTTGTGCTTATCTCTGGTAAATATAAAGGACTCAAAAG 468
Db 181 CGGTGTCCTGGCAATCTCTCTGTTGTGCTTATCTCTGGTAAATATAAAGGACTCAAAAG 240
QY 469 CGTGGAAATATCTATCTTAAACTGGCAGTTCTAATCTGTTCTGTTCTGTTACCT 528
Db 241 CGTGGAAATATCTATCTTAAACTGGCAGTTCTAATCTGTTCTGTTCTGTTACCT 300
QY 529 GCCCTTCCTGGGCTCATGCTGGGGCGATCCCATGTGTAATAATCTCATTGGACTGTACTT 588
Db 301 GCCCTTCCTGGGCTCATGCTGGGGCGATCCCATGTGTAATAATCTCATTGGACTGTACTT 360
QY 589 CGTGGGCTGTACAGTGAGACATTTTTCATATTCCTGATTCCTGATGTCGAAAGTACTAGT 648
Db 361 CGTGGGCTGTACAGTGAGACATTTTTCATATTCCTGATTCCTGATGTCGAAAGTACTAGT 420
QY 649 GTTTTGGCAAGGGCACTTTTCTCAGCCAGGAGGAGGTGCTGTCGATCATATAC 708
Db 421 GTTTTGGCAAGGGCACTTTTCTCAGCCAGGAGGAGGTGCTGTCGATCATATAC 480
QY 709 AAGTGTCTGGGATGGGTAAACAGCCATCTCGGCCACTTTTGGCTGAATAGTGTGTTATAA 768
Db 481 AAGTGTCTGGGATGGGTAAACAGCCATCTCGGCCACTTTTGGCTGAATAGTGTGTTATAA 540
QY 769 ACTCAGATGGAAGACCAAGATACAAATGATGATGATGATGATGATGATGATGATGATGAT 828
Db 541 ACTCAGATGGAAGACCAAGATACAAATGATGATGATGATGATGATGATGATGATGATGAT 600
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Db 601 TGATGAGACATCTGGAGCAATTTCTGACTTTTAAATGAACATTTGGTTCTGTCT 660
QY 889 CCCCCTATTATTTTACATTTCTCTATGTGCAATGAGAAAAACACTAAGTTTCAGGGA 948
Db 661 CCCCCTATTATTTTACATTTCTCTATGTGCAATGAGAAAAACACTAAGTTTCAGGGA 720
QY 949 GCAGAGGTATAGCTTTTCAAGCTGTTTTCGATTAATGATGATGATGATGATGATGATGATG 1008
Db 721 GCAGAGGTATAGCTTTTCAAGCTGTTTTCGATTAATGATGATGATGATGATGATGATGATG 780
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RESULT 11

US-10-223-082-15
; Sequence 15, Application US/10223082
; Publication No. US20030191059A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe P.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C3
; CURRENT APPLICATION NUMBER: US/10/223,082

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QY 1069 CTGCAAGAGCAGCTACAAATCTGGACAAAAGTGTTCACATCACTAAACTCATGCCACCCAC 1128
Db 841 CTGCAAGAGCAGCTACAAATCTGGACAAAAGTGTTCACATCACTAAACTCATGCCACCCAC 900
QY 1129 CCATGCTGCATCAACCCCTCTCTGTATGCGTTTCTTGATGGGACATTTAGCAATACCT 1188
Db 901 CCATGCTGCATCAACCCCTCTCTGTATGCGTTTCTTGATGGGACATTTAGCAATACCT 960
QY 1189 CTGCGCGCTGTTTCCCATCTGCGTAGTAACACCCCACTTCAACCCGAGGAGCTCTGCACA 1248
Db 961 CTGCGCGCTGTTTCCCATCTGCGTAGTAACACCCCACTTCAACCCGAGGAGCTCTGCACA 1020
QY 1249 AGGCACATCGAGGGAAGAACCTGCACATTTCCACCGAAGTGTAAACTAGCATCCACCAAT 1308
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Db 1261 ACCACTTCTCATAGTGTGGATAGACTAGTCTCAATTTCTCTGAGAGAAACCTAAGCG 1320
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Db 1321 CGGAATTTGCTTAAGATCACAATTAAGTGGAGAGTGGAGAGTGGTCTCCAGCCCTGCT 1380
QY 1609 AGCATTTGCTCAGAGCCCTACGCTTGCTCCAGAACATCAAACTCCAAACCCCTGGGGACAAA 1668
Db 1381 AGCATTTGCTCAGAGCCCTACGCTTGCTCCAGAACATCAAACTCCAAACCCCTGGGGACAAA 1440
QY 1669 CGACATGAATAAATGTAATTTTAAACATC 1698
Db 1441 CGACATGAATAAATGTAATTTTAAACATC 1470
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; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-223-082-15

Query Match      86.5%; Score 1468.4; DB 16; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 229 GGAGCTCAGCCAGTGGGAGTCTGAAGATGGCCAAATTACACCTGGCACCAGAGTGA 288
Db 1 GGAGCTCAGCCAGTGGGAGTCTGAAGATGGCCAAATTACACCTGGCACCAGAGTGA 60

Qy 289 ATATGATGTCTCATAGAAGGTGAATCTGGAGAGCGATGAGCGAGCAATGTGACAAAGTA 348
Db 61 ATATGATGTCTCATAGAAGGTGAATCTGGAGAGCGATGAGCGAGCAATGTGACAAAGTA 120

Qy 349 TGAGGCCAGGCACTCTCAGCCAGCTGGTGCCATCACTCTGCTGTGTGTGTGTGTGTGT 408
Db 121 TGAGGCCAGGCACTCTCAGCCAGCTGGTGCCATCACTCTGCTGTGTGTGTGTGTGTGT 180

Qy 409 CGGTGTCTGGCAATCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 468
Db 181 CGGTGTCTGGCAATCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240

Qy 469 CGTGGAAATATCTATCTTCTAAACTTGGCAGTCTTAACTGTGTGTGTGTGTGTGTGTGT 528
Db 241 CGTGGAAATATCTATCTTCTAAACTTGGCAGTCTTAACTGTGTGTGTGTGTGTGTGTGT 300

Qy 529 GCCCTTCTGGGCTCATGTCTGGGGCGATCCCATGTGTAAATTTCTCATTTGAGCTGTACT 588
Db 301 GCCCTTCTGGGCTCATGTCTGGGGCGATCCCATGTGTAAATTTCTCATTTGAGCTGTACT 360

Qy 589 CGTGGGCTGTACAGTGAGACATTTTCAATGGCTTCTGACGTGCGAAGGTACCTAGT 648
Db 361 CGTGGGCTGTACAGTGAGACATTTTCAATGGCTTCTGACGTGCGAAGGTACCTAGT 420

Qy 649 GTTTTGTGCAAGGGCAACTTTTCTCAGCCAGAGGAGGTGCTGCTGGCATCATTTAC 708
Db 421 GTTTTGTGCAAGGGCAACTTTTCTCAGCCAGAGAGGAGGTGCTGCTGGCATCATTTAC 480

Qy 709 AAGTGTCTGGCATGGGTAAACAGCCATTTCTGGCCACTTTGCTCCCTGAATAGCTGTGTATTA 768
Db 481 AAGTGTCTGGCATGGGTAAACAGCCATTTCTGGCCACTTTGCTCCCTGAATAGCTGTGTATTA 540

Qy 769 ACCTCAGATGGAGACAGCAATATACAGTGTGTGATTTAGCAGAACTCCCTTCTGCGCAGC 828
Db 541 ACCTCAGATGGAGACAGCAATATACAGTGTGTGATTTAGCAGAACTCCCTTCTGCGCAGC 600
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Qy 829 TGATGAGACATTTCTGGAAGCAATTTCTGACTTTTAAAAATGAACAATTTGGTCTTGTCTCT 888
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Qy 949 GCAGAGATATAGCTTTTCAAGCTGTGTTTTTGGCATAAATGCTGTCTTCTTCTGTGTGTG 1008
Db 721 GCAGAGATATAGCTTTTCAAGCTGTGTTTTTGGCATAAATGCTGTCTTCTTCTGTGTGTG 780

Qy 1009 GCGGCCCTACAAATATTGCAATTTTCTGTCTCCACTTTTCAAAAGAACACTTTCTCCCTGAGTGA 1068
Db 781 GCGGCCCTACAAATATTGCAATTTTCTGTCTCCACTTTTCAAAAGAACACTTTCTCCCTGAGTGA 840

Qy 1069 CTGCAAGAGCAGCTACAATCTGCAAAAAAGTGTTCACATCACTAAACTCATCGCCACCAC 1128
Db 841 CTGCAAGAGCAGCTACAATCTGCAAAAAAGTGTTCACATCACTAAACTCATCGCCACCAC 900

Qy 1129 CCACTCTGTCATCAACCCCTCTCTCTGTATGCTTTTCTGTGGGACATTTTATAGCAAAATACCT 1188
Db 901 CCACTCTGTCATCAACCCCTCTCTCTGTATGCTTTTCTGTGGGACATTTTATAGCAAAATACCT 960

Qy 1189 CTGCGCTGTCTTCCATCTGCTAGTAAACACCCCACTTTCAACCCAGGGGGCAGTCTGCACA 1248
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Qy 1249 AGGCACATCGAGGGAAGAACCTGACCATTTCCACCGAAGTGTAACTAGCATTCACCAAAAT 1308
Db 1021 AGGCACATCGAGGGAAGAACCTGACCATTTCCACCGAAGTGTAACTAGCATTCACCAAAAT 1080

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Db 1081 GCAAGAAGATAAACATGATTTTTCATCTTCTGCAATTTTTCATGTAAATTTTCTACAC 1140

Qy 1369 ATTTGTATACAAATCGGATACAGGAAGAAAAAGGAGAGGTGAGCTAACTTTTGTCTAAGC 1428
Db 1141 ATTTGTATACAAATCGGATACAGGAAGAAAAAGGAGAGGTGAGCTAACTTTTGTCTAAGC 1200

Qy 1429 ACTGAATTTGTCTCAGGCAACCGTGCAAGGCTCTTTTACAAACGTGAGCTCTTCTGCTCTCT 1488
Db 1201 ACTGAATTTGTCTCAGGCAACCGTGCAAGGCTCTTTTACAAACGTGAGCTCTTCTGCTCTCT 1260

Qy 1489 ACCACTTGTCCATGTGTGATAGGACTAGTCTCTCTCTCTGAGAGAAACCTAAGGCG 1548
Db 1261 ACCACTTGTCCATGTGTGATAGGACTAGTCTCTCTCTCTGAGAGAAACCTAAGGCG 1320

Qy 1549 CGGAATTTGTCTAAGATCACTTAACTAGGAAGTGCAGAACTGATTTCTCAGCCCTTGGT 1608
Db 1321 CGGAATTTGTCTAAGATCACTTAACTAGGAAGTGCAGAACTGATTTCTCAGCCCTTGGT 1380

Qy 1609 AGCATTTGTCTCAGAGCTTACGCTTGGTCCAGAACTCAAACTCCAAACCTCTGGGGACAAA 1668
Db 1381 AGCATTTGTCTCAGAGCTTACGCTTGGTCCAGAACTCAAACTCCAAACCTCTGGGGACAAA 1440

Qy 1669 CGACATGAATAAATGATTTTAAACATC 1698
Db 1441 CGACATGAATAAATGATTTTAAACATC 1470
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RESULT 12
US-10-305-654-15
; Sequence 15, Application US/10305654
; Publication No. US20030224994A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hans-Peter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
```

; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scott A.
; APPLICANT: Pan, J.
; APPLICANT: Paoni, N. F.
; APPLICANT: Stephan, J-P F.
; APPLICANT: Watanabe, C.K.
; APPLICANT: Wood, W.I.
; APPLICANT: Williams, P.M.
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235R1C1
; CURRENT APPLICATION NUMBER: US/10/305,654
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homosapiens
US-10-305-654-15

Query Match 86.5%; Score 1468.4; DB 17; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 229 GGAGCTCAGCCAGTGGGCGAGTCTGAAGATGGCCAAATACAGCTGGGCAACGAGAGATGA 288
Db 1 GGAGCTCAGCCAGTGGGCGAGTCTGAAGATGGCCAAATACAGCTGGGCAACGAGAGATGA 60

QY 289 ATATGATGTCCTCATAGAGGTGAACCTGGAGAGCGATGAGGAGAGGATGACAGTGA 348
Db 61 ATATGATGTCCTCATAGAGGTGAACCTGGAGAGCGATGAGGAGAGGATGACAGTGA 120

QY 349 TGACGCCAGGCACTCTCAGCCAGCTGGTGGCATCACTCTGCTCTGCTGTGTGTGTGAT 408
Db 121 TGACGCCAGGCACTCTCAGCCAGCTGGTGGCATCACTCTGCTCTGCTGTGTGTGAT 180

QY 409 CGGTGTCGGAACAATCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 468
Db 181 CGGTGTCGGAACAATCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240

QY 469 CGTGGAAATATCTATCTTAACTTGGCAGTTTCTAACTTGGCAGTTTCTAACTTGGCAGTTT 528
Db 241 CGTGGAAATATCTATCTTAACTTGGCAGTTTCTAACTTGGCAGTTTCTAACTTGGCAGTTT 300

QY 529 GGCCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTT 588
Db 301 GGCCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTT 360

QY 589 CGTGGCCCTGTACAGTGAGACATTTTTCATTTGCTTCTGCTTCTGCTGCAAGGTAAGTCT 648
Db 361 CGTGGCCCTGTACAGTGAGACATTTTTCATTTGCTTCTGCTTCTGCTGCAAGGTAAGTCT 420

QY 649 GTTTTGGCAAGGCAACTTTTCTCAGCCAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 708
Db 421 GTTTTGGCAAGGCAACTTTTCTCAGCCAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 480

QY 709 AAGTGTCTGGCATGGGTAAACGCCATTTCTGGCCACTTTTGGCCCTGAATAGCTGTTTATAA 768
Db 481 AAGTGTCTGGCATGGGTAAACGCCATTTCTGGCCACTTTTGGCCCTGAATAGCTGTTTATAA 540

QY 769 ACTCAGATGGAAGACCAAGATATACAAAGTGTGATTTAGAGAACTCCCTTCTGCGCAGC 828
Db 541 ACTCAGATGGAAGACCAAGATATACAAAGTGTGATTTAGAGAACTCCCTTCTGCGCAGC 600

QY 829 TGATGAGACATCTGGAAGCATTTCTGCTTTTAAATGAACATTTTCGCTTCTGCTGCT 888
Db 601 TGATGAGACATCTGGAAGCATTTCTGCTTTTAAATGAACATTTTCGCTTCTGCTGCT 660

QY 889 CCCCTTATTTTATTTTATCTTCTATGTGCAATGAGAAAAACAACTAAGGTTTCAGGGA 948
Db 661 CCCCTTATTTTATTTTATCTTCTATGTGCAATGAGAAAAACAACTAAGGTTTCAGGGA 720

QY 949 GCAGAGGTATAGCCCTTTTCAAGCTTTTGTGTCCTAATAGTGTAGTCTTCTTCTGATG 1008
Db 721 GCAGAGGTATAGCCCTTTTCAAGCTTTTGTGTCCTAATAGTGTAGTCTTCTTCTGATG 780

QY 1009 GCGCCCTTACAAATATTGCAATTTTCTGTCACATTTTCAAGAAACACTTCTCCCTGAGTGA 1068
Db 781 GCGCCCTTACAAATATTGCAATTTTCTGTCACATTTTCAAGAAACACTTCTCCCTGAGTGA 840

QY 1069 CTGCAAGAGCAGCTCAATCTGGAACAAAGTGTTCACATCACTAACTCATCGCCACCAC 1128
Db 841 CTGCAAGAGCAGCTCAATCTGGAACAAAGTGTTCACATCACTAACTCATCGCCACCAC 900

QY 1129 CCATCTGTCATCAACCTCTCTGATGCGTTTCTTGTGATGGACATTTAGCAAAATACCT 1188
Db 901 CCATCTGTCATCAACCTCTCTGATGCGTTTCTTGTGATGGACATTTAGCAAAATACCT 960

QY 1189 GTCCGCTGTTTCCATCTGCGTAGTAACAACCCACTTCAACCCAGGGGCGAGTCTGACACA 1248
Db 961 GTCCGCTGTTTCCATCTGCGTAGTAACAACCCACTTCAACCCAGGGGCGAGTCTGACACA 1020

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Db 1081 GCAGAAGATTAACATGGATTTTTCATCTTCTGCAATTTTTCATGTAATTTTCTACAC 1140

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Db 1141 ATTTGTATACAAATTCGGATACAGGAAGAAAGGAGAGGTGAGCTAACATTTGCTAAGC 1200

QY 1429 ACTGAATTTGCTCAGGCAACCGTCAAGGCTTTTCAAACTGAGCTCTCTTCCGCTCTCT 1488
Db 1201 ACTGAATTTGCTCAGGCAACCGTCAAGGCTTTTCAAACTGAGCTCTCTTCCGCTCTCT 1260

QY 1489 ACCACTTGTCCATAGTGTGATAGTAGTCTCATTTCTCTGAGAAAGAACTAAGCG 1548
Db 1261 ACCACTTGTCCATAGTGTGATAGTAGTCTCATTTCTCTGAGAAAGAACTAAGCG 1320

QY 1549 CGGAAATTTGCTAAGATCACCTTAAGTAGGAGTGGCAAACTGATTTCTCCAGCCCTGCT 1608
Db 1321 CGGAAATTTGCTAAGATCACCTTAAGTAGGAGTGGCAAACTGATTTCTCCAGCCCTGCT 1380

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Db 1381 AGCATTGCTCAGAGCTTACGCTTGGTCCAGAACTCAAACTCCAAAACCTGGGGACAAA 1440

QY 1669 CGACATGAATTAATGATTTTAAACATC 1698
Db 1441 CGACATGAATTAATGATTTTAAACATC 1470

RESULT 13
US-10-081-056-15
; Sequence 15, Application US/10081056
; Publication No. US20040043927A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scott A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey

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; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C1
; CURRENT APPLICATION NUMBER: US/10/081,056
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/230,978
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/000,000
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 09/664,610
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/242,922
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/709,238
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30952
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/767,609
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 09/796,498
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: US 09/802,706
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/808,689
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 09/816,744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 09/828,366
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 09/854,208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/854,280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/866,034
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/US01/17092
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/870,574

; Query Match 86.5%; Score 1468.4; DB 18; Length 1475;
; Best Local Similarity 99.9%; Pred. No. 0;
; Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 229 GGAGCTCAGCCAGTGGGCGAGTCTGAAGATGGCCAATTACACGCTGSCACACGAGGATGA 288
Db 1 GGAGCTCAGCCAGTGGGCGAGTCTGAAGATGGCCAATTACACGCTGSCACACGAGGATGA 60
QY 289 ATATGATGTCTCATAGAAGTGAACCTGGAGAGCGATGAGGCGAGCAATGTGCAAGTA 348
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Db 121 TGACGCCAGGCACTCTCAGCCAGCTGGTGCCATCCTCTGCTCTGCTGCTGCTGCTGAT 180
QY 409 CGGTGCTCTGGCAATCTCTCTGCTGCTTATCTCTGTTAAATATATAAGGACTCAAAACG 468
Db 181 CGGTGCTCTGGCAATCTCTCTGCTGCTTATCTCTGTTAAATATATAAGGACTCAAAACG 240
QY 469 CGTGAAAAATATCTATCTTTCTAAACTTGGCAGTTTCTAACTTGTGTTCTTGTCTTACCCCT 528
Db 241 CGTGAAAAATATCTATCTTTCTAAACTTGGCAGTTTCTAACTTGTGTTCTTGTCTTACCCCT 300
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QY 649 GTTTTTCACAAAGGCAACTTTTTCTCAGCAGGAGGGGTGCCCTGTGGCATCATTTAC 708
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QY 709 AAGTGTCTGGCATGGGTAACAGCCATTTCTGGCCACTTTGGCTGTAATAGTGTGTTATAA 768
Db 481 AAGTGTCTGGCATGGGTAACAGCCATTTCTGGCCACTTTGGCTGTAATAGTGTGTTATAA 540
QY 769 ACCTCAGATGGGAAGACCAAGATACAAAGTGTCAATTTAGCAGCACTCCCTTCTGCGCAGC 828
Db 541 ACCTCAGATGGGAAGACCAAGATACAAAGTGTCAATTTAGCAGCACTCCCTTCTGCGCAGC 600
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Db 661 CCCCCTATTTATTTTACATTTCTCTATGTGCAATGAGAAAAACAATAGGTTTCAGGGA 720
QY 949 GCAGAGGTATAGCCCTTTTCAAGCTTGTGTTTGGCCATATGTTCTTCTCTCTGATGTC 1008
Db 721 GCAGAGGTATAGCCCTTTTCAAGCTTGTGTTTGGCCATATGTTCTTCTCTCTGATGTC 780
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Qy	1129	CCACTGCTGCATCAACCCCTCTCTGTATGCGTTTCTTGATGGACATTTAGCAAAATCCT	1188
Db	901	CCACTGCTGCATCAACCCCTCTCTGTATGCGTTTCTTGATGGACATTTAGCAAAATCCT	960
Qy	1189	CTGCGCGCTGTTCCATCTCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACA	1248
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Qy	1249	AGGCACATCGAGGGAAGAACCTGACCATCTCCACCGAAGTGTAAACTAGCATCCACAAAT	1308
Db	1021	AGGCACATCGAGGGAAGAACCTGACCATCTCCACCGAAGTGTAAACTAGCATCCACAAAT	1080
Qy	1309	GCAAGAGATAAACATGGAATTTTCATCTTCTGCAATTTATCATGTAAATTTCTACAC	1368
Db	1081	GCAAGAGATAAACATGGAATTTTCATCTTCTGCAATTTATCATGTAAATTTCTACAC	1140
Qy	1369	ATTGTGTATCAAAATCGGATACAGGAAGAAAGGAGAGGTGAGCTAAATTTGCTAAGC	1428
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Qy	1429	ACTGAATTTGCTCAGGCAACCGTGCAAGGCTCTTTTACAAAGTGAGCTCTTCGCTCCT	1488
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Qy	1489	ACCACCTGTCATAGTGTGGATAGGACTAGTCTCATTTCTCGAAGAAACTAAGGCG	1548
Db	1261	ACCACCTGTCATAGTGTGGATAGGACTAGTCTCATTTCTCGAAGAAACTAAGGCG	1320
Qy	1549	CGGAAATTTGCTAAGATCACTTAACCTAGGAAGTGGCAAACTGATTTCTCCAGCCCTGCT	1608
Db	1321	CGGAAATTTGCTAAGATCACTTAACCTAGGAAGTGGCAAACTGATTTCTCCAGCCCTGCT	1380
Qy	1609	AGCATTTGCTCAGAGCTTACGTTGGTCCAGAACATCAAACTCCAAACCCCTGGGACAAA	1668
Db	1381	AGCATTTGCTCAGAGCTTACGTTGGTCCAGAACATCAAACTCCAAACCCCTGGGACAAA	1440
Qy	1669	CGACATGAATAAATCTATTTTAAACATC	1698
Db	1441	CGACATGAATAAATCTATTTTAAACATC	1470
RESULT 14			
US-10-225-567A-353			
; Sequence 353, Application US/10225567A			
; Publication No. US20030113798A1			
; GENERAL INFORMATION:			
; APPLICANT: LifeSpan Biosciences			
; APPLICANT: Brown, Joseph P.			
; APPLICANT: Burner, Glenna C.			
; APPLICANT: Roush, Christine L.			
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS			
; FILE REFERENCE: 1920-4-4			
; CURRENT APPLICATION NUMBER: US/10/225,567A			
; CURRENT FILING DATE: 2001-12-19			
; PRIOR APPLICATION NUMBER: 60/257,144			
; PRIOR FILING DATE: 2000-12-19			
; NUMBER OF SEQ ID NOS: 2292			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 353			
; LENGTH: 1645			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-225-567A-353			
Query Match 85.7%; Score 1455.2; DB 15; Length 1645;			
Best Local Similarity 99.8%; Pred. No. 0;			

Matches 1457; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
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Db	185	CCACAGGCGAGTCTGAAGATGGCCCAATTTACAGCTGGCACCCAGAGGATGAATATGTC	244
Qy	239	CTCATAGAAGGTGAATCTGGAGAGCGATCAGGCAGAGCAATGTGACAAAGTATGACGCCCAAG	358
Db	245	CTCATAGAAGGTGAATCTGGAGAGCGATCAGGCAGAGCAATGTGACAAAGTATGACGCCCAAG	304
Qy	359	GCATCTCTCAGCCCGAGCTGGTGCATCACTCTGCTCTGCTGTGTTTGTGATCGGTCTCTGG	418
Db	305	GCATCTCTCAGCCCGAGCTGGTGCATCACTCTGCTCTGCTGTGTTTGTGATCGGTCTCTGG	364
Qy	419	GACAACTCTCTGTTGTGCTTATCTCTGTATAAATAAAGGACTCAAAACCGTGGAAAT	478
Db	365	GACAACTCTCTGTTGTGCTTATCTCTGTATAAATAAAGGACTCAAAACCGTGGAAAT	424
Qy	479	ATCTATCTTCTAAACTTGGCAGTTTCTAACTTGTGTTTCTTCTTACCTGCTTCTGG	538
Db	425	ATCTATCTTCTAAACTTGGCAGTTTCTAACTTGTGTTTCTTCTTACCTGCTTCTGG	484
Qy	539	GCTCATGCTGGGGCGATCCCATGTGTAAAAATTTCTCATTTGGACTGTACTTCTGTGGCCTG	598
Db	485	GCTCATGCTGGGGCGATCCCATGTGTAAAAATTTCTCATTTGGACTGTACTTCTGTGGCCTG	544
Qy	599	TACAGTGAGACATTTTCAATTTGCCCTTCTGACTGTGCAAGGTAAGTGTGTTTGTGAC	658
Db	545	TACAGTGAGACATTTTCAATTTGCCCTTCTGACTGTGCAAGGTAAGTGTGTTTGTGAC	604
Qy	659	AAGGCAACTTTTCTCAGCCAGGAGGAGGTGCCCTGTGTCATCATTTACAAAGTGTCTCTG	718
Db	605	AAGGCAACTTTTCTCAGCCAGGAGGAGGTGCCCTGTGTCATCATTTACAAAGTGTCTCTG	664
Qy	719	GCATGGGTAAACAGCCATTTCTGGCCACTTTTGGCTGAATACTGCTGTTTATAAACCTCAGATG	778
Db	665	GCATGGGTAAACAGCCATTTCTGGCCACTTTTGGCTGAATACTGCTGTTTATAAACCTCAGATG	724
Qy	779	GAAGCCAGAAATACAAAGTGTGCATTTAGCAGAACTCCCTTCTGCGAGCTGATGAGACA	838
Db	725	GAAGCCAGAAATACAAAGTGTGCATTTAGCAGAACTCCCTTCTGCGAGCTGATGAGACA	784
Qy	839	TTCTGGAAGCATTTTCTGACTTTAAATAATGAACATTTTCGGTTCTTGTCTCTCCCTCTATT	898
Db	785	TTCTGGAAGCATTTTCTGACTTTAAATAATGAACATTTTCGGTTCTTGTCTCTCCCTCTATT	844
Qy	899	ATTTTACATTTCTCTATGTCAAATGAGAAAAACACTAAAGTTTCAGGAGCAGAGGTAT	958
Db	845	ATTTTACATTTCTCTATGTCAAATGAGAAAAACACTAAAGTTTCAGGAGCAGAGGTAT	904
Qy	959	AGCCTTTTCAAGCTTGTGTTTGGCAATATGTTAGTCTTCTTCTGATGTGGGCGCCCTAC	1018
Db	905	AGCCTTTTCAAGCTTGTGTTTGGCAATATGTTAGTCTTCTTCTGATGTGGGCGCCCTAC	964
Qy	1019	AATATTGCAATTTTCTCTGCTCCACTTTTCAAGAAACACTTCTCCCTGAGTGACTGCAAGAGC	1078
Db	965	AATATTGCAATTTTCTCTGCTCCACTTTTCAAGAAACACTTCTCCCTGAGTGACTGCAAGAGC	1024
Qy	1079	AGCTACAACTCGGACAAAGTGTTCACATCACTAAACTCATCGCCACCAACCCACTGCTGC	1138
Db	1025	AGCTACAACTCGGACAAAGTGTTCACATCACTAAACTCATCGCCACCAACCCACTGCTGC	1084
Qy	1139	ATCAACCTCTCTGTTATGCGTTTCTTGATGGGACATTTAGCAATATCTCTGCGCTGT	1198
Db	1085	ATCAACCTCTCTGTTATGCGTTTCTTGATGGGACATTTAGCAATATCTCTGCGCTGT	1144
Qy	1199	TTCCATCTGCTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCAACAGGCAATCG	1258
Db	1145	TTCCATCTGCTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCAACAGGCAATCG	1204
Qy	1259	AGGGAAGAACCTGACCAATTCACCGAAGTGTAAACTAGCATCCACCAAAATGCAAGAA	1318
Db	1205	AGGGAAGAACCTGACCAATTCACCGAAGTGTAAACTAGCATCCACCAAAATGCAAGAA	1264

Qy	1559	TCTAAGATCACTTAAGTAGGAAAGTGGCAGAACTGATTCTCCAGCCCTGGTAGCATTTGCT	1618
Db	97944	TCTAAGATCACATAACTAGGAAAGTGGCAGAACTGATTCTCCAGCCCTGGTAGCATTTGCT	98003
Qy	1619	CAGAGCTACGCTTGGTCCAGAACATCCAAACCCCTGGGACAAACGACATGAAA	1678
Db	98004	CAGAGCTACGCTTGGTCCAGAACATCCAAACCCCTGGGACAAACGACATGAAA	98063
Qy	1679	TAAATGTATTTTAAACATC	1698
Db	98064	TAAATGTATTTTAAACATC	98083

Search completed: June 18, 2005, 20:05:12
Job time : 1076 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 18, 2005, 06:34:54 ; Search time 666.776 Seconds
(without alignments)
9615.040 Million cell updates/sec

Title: US-10-623-472-32

Perfect score: 1083

Sequence: 1 atggataactacacagtggc.....aaaggcaggataataataa 1083

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1980s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1083	100.0	1083	6	ABSS52093 Mouse CCR
2	1076.6	99.4	1083	12	ADO30354 Mouse GPC
3	1076.6	99.4	2045	6	AAD32931 Mus muscu
4	423.2	39.1	1646	13	ADQ38349 Human SNP
5	423.2	39.1	1776	13	ADQ38350 Human SNP
6	422	39.0	1140	12	ACH89585 Human gen
7	422	39.0	1475	6	ABL88079 Human PRO
8	422	39.0	1475	6	ABL95568 Human ang
9	422	39.0	1475	10	ADD10304 Human sec
10	422	39.0	1475	10	ADD11264 Human sec
11	422	39.0	1475	12	ADD37057 Human sec
12	422	39.0	1475	12	ADH41265 Human sec
13	422	39.0	1475	12	ADH43448 Human PRO
14	422	39.0	1475	12	ADK82793 Human PRO
15	422	39.0	1645	8	ABZ42782 Human che
16	422	39.0	1645	11	ADN95729 Human BEC
17	422	39.0	1645	13	ADP24442 Human poly
18	422	39.0	1645	13	ADST75309 Human CCR
19	422	39.0	1698	12	ADP13564 Renal cel
20	422	39.0	143040	11	ABD20648 Human pul

21	422	39.0	143067	11	ABD20815	Abd20815 Human pul
22	422	39.0	143068	3	AAA34983	Aaa34983 Human ade
23	422	39.0	143068	3	AAA35150	Aaa35150 Human ade
24	422	39.0	143068	3	AAF21272	Aaf21272 Human low
25	422	39.0	143068	3	AAF21105	Aaf21105 Human low
26	422	39.0	143068	6	ABL68124	AbL68124 Ovary can
27	422	39.0	143068	6	ABT11034	Abt11034 Human bre
28	422	39.0	143068	10	ABZ96966	Abz96966 Human nuc
29	422	39.0	143068	10	ABZ96799	Abz96799 Human nuc
30	422	39.0	149412	3	AAA35151	Aaa35151 Human ade
31	422	39.0	152739	11	ABD20816	Abd20816 Human pul
32	422	39.0	152740	3	AAF21273	Aaf21273 Human low
33	422	39.0	152740	10	ABZ96967	Abz96967 Human nuc
34	421.6	38.9	1270	10	ACA56158	Aca56158 Human eig
35	421.6	38.9	1270	12	ADI55954	Adi55954 Human pol
36	421.2	38.9	1316	2	AAT99543	Aat99543 Human che
37	420.4	38.8	1547	2	AAV15419	Aav15419 Human mac
38	420.4	38.8	1547	10	ABX95937	Abx95937 Human mon
39	420.4	38.8	1547	12	ADQ67844	Adq67844 Human CDN
40	412.4	38.1	1035	6	ABSS52092	Abss52092 Human CCR
41	412.4	38.1	1035	12	ADQ30063	Adq30063 Human GPC
42	412	38.0	1251	11	ADP03560	Adp03560 Human GPC
43	398.4	36.8	1050	2	AAV04641	Aav04641 cDNA enco
44	398.4	36.8	1050	6	AAAS17436	Aaas17436 Human CDN
45	398.4	36.8	1050	6	AAD42836	Aad42836 Human G-p

ALIGNMENTS

RESULT 1

ABSS52093

ID ABSS52093 standard; cDNA; 1083 BP.

AC ABSS52093;

XX 05-NOV-2002 (first entry)

DT Mouse CCR12 cDNA.

DE Mouse CCR12 cDNA.

XX Mouse; CCR12; gene; ss; chemokine receptor; L-CCR; MCP-1; HBK cell;

KW Monocyte Chemoattractant Protein-1; brain glial cell; ischaemia; asthma;

KW inflammatory disease; degenerative brain disease; Alzheimer's disease;

KW multiple sclerosis; neurodegenerative disease; neuroinflammatory disease;

KW allergic encephalitis; chronic obstructive pulmonary disease;

KW obstructive airway disease; neuroprotective; antiinflammatory.

XX Mus sp.

OS Mus sp.

XX WO200257779-A2.

XX 25-JUL-2002.

XX 18-JAN-2002; 2002WO-NL000039.

XX 18-JAN-2001; 2001EP-00200181.

XX (UYGR-) RIJKSUNIV GRONINGEN.

XX Boddeke EHWGM, Biber K;

XX WPI; 2002-599725/64.

XX Identifying compounds for treating inflammatory or degenerative brain

XX diseases, comprises testing the compound for its capacity to modulate or

XX mimic Monocyte Chemoattractant Protein-1 binding with a chemokine

XX receptor.

XX Disclosure; Fig 8; 45pp; English.

XX The invention relates to identifying a candidate drug compound comprising

XX testing the compound for its capacity to modulate or mimic Monocyte

XX Chemoattractant Protein-1 (MCP-1) binding with a chemokine receptor

CC capable of being expressed on brain glial cells and is known in the mouse
 CC as L-CCR or in humans as CRAW-B. The chemokine receptor expressed in a
 CC cultured cell comprising the cell transfected with a nucleic acid and a
 CC HEK cell, is useful in identifying a candidate drug compound for treating
 CC inflammatory or degenerative brain disease, e.g. ischaemia, Alzheimer's
 CC disease or multiple sclerosis. The agonist or antagonist is useful in the
 CC preparation of the pharmaceutical composition useful in treating
 CC neurodegenerative and neuroinflammatory diseases such as allergic
 CC encephalitis and chronic obstructive pulmonary disease and obstructive
 CC airway diseases such as asthma. This sequence represents mouse L-CCR
 CC cDNA, also known as CCR12
 XX
 SQ

Sequence 1083 BP; 237 A; 294 C; 274 G; 278 T; 0 U; 0 Other;

Query Match 100.0%; Score 1083; DB 6; Length 1083;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1083; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGATAACTACACAGTGGCCCGGACGATGAATATGATCTCTAATCTTAGACGACTAC 60
 DB 1 ATGGATAACTACACAGTGGCCCGGACGATGAATATGATCTCTAATCTTAGACGACTAC 60
 QY 61 CTGGACAACAGTGGCCCGGACCAAGTTCCGCGCCCGGAGTTCTCTCCCGCCAGCAGGTG 120
 DB 61 CTGGACAACAGTGGCCCGGACCAAGTTCCGCGCCCGGAGTTCTCTCCCGCCAGCAGGTG 120
 QY 121 CTGCAAGTCTCTGCGCGGTGTTTGGGTGGTCTCTTGACAAACGTGCTGGCGGTGTTT 180
 DB 121 CTGCAAGTCTCTGCGCGGTGTTTGGGTGGTCTCTTGACAAACGTGCTGGCGGTGTTT 180
 QY 181 ATCTTGTTGAATACAAAGACATCAAGATCTGGGAACATCTACTTCTTAAACCTGGCA 240
 DB 181 ATCTTGTTGAATACAAAGACATCAAGATCTGGGAACATCTACTTCTTAAACCTGGCA 240
 QY 241 CTTTCAAACCTGTGTTTCTCTGCTTCCCGTCCCGTTCTGGGCCCATCTATGACGACACGGG 300
 DB 241 CTTTCAAACCTGTGTTTCTCTGCTTCCCGTCCCGTTCTGGGCCCATCTATGACGACACGGG 300
 QY 301 GAAAGCCCTGGCAACGGGACCTGTAAAGTTCTTGTGGACTCACCTCTGGGCTTATAC 360
 DB 301 GAAAGCCCTGGCAACGGGACCTGTAAAGTTCTTGTGGACTCACCTCTGGGCTTATAC 360
 QY 361 AGGAGGTGTTTCCACATCTCTCTCTGTCGCAAGATACAGGGTGTTCCTCCAGGG 420
 DB 361 AGGAGGTGTTTCCACATCTCTCTCTGTCGCAAGATACAGGGTGTTCCTCCAGGG 420
 QY 421 CGACTGGCCCTCCATCTTTCAGCAGAGTGTCTTGTGGTATTTGTGGTGCATCTCTGGCATGG 480
 DB 421 CGACTGGCCCTCCATCTTTCAGCAGAGTGTCTTGTGGTATTTGTGGTGCATCTCTGGCATGG 480
 QY 481 GCAATGGCTACTGGGCTCTCTTGGCCGAGTCTGTGTTTTATGAGCCTCGGATGGAAGA 540
 DB 481 GCAATGGCTACTGGGCTCTCTTGGCCGAGTCTGTGTTTTATGAGCCTCGGATGGAAGA 540
 QY 541 CAGAAACACAGTGTGCTTTGGCAACCTCCTCTTGGCAATCGAAGCGCGCTCTGG 600
 DB 541 CAGAAACACAGTGTGCTTTGGCAACCTCCTCTTGGCAATCGAAGCGCGCTCTGG 600
 QY 601 AAGTACGTTCTGACGTCACAAATGATCATCTGTACTTCTCTCTCTGCTGGTTTTT 660
 DB 601 AAGTACGTTCTGACGTCACAAATGATCATCTGTACTTCTCTCTCTGCTGGTTTTT 660
 QY 661 ATAATCTGCTGACGTAAGAGAGAGGAGAGCTTTCAGGAGAGACAGTACGACCTC 720
 DB 661 ATAATCTGCTGACGTAAGAGAGAGGAGAGCTTTCAGGAGAGACAGTACGACCTC 720
 QY 721 CACAAGCGGCTCTGTGTATAACGGGCGTGTCTCTTTTGTGGGGCGCTTCAACACT 780
 DB 721 CACAAGCGGCTCTGTGTATAACGGGCGTGTCTCTTTTGTGGGGCGCTTCAACACT 780
 QY 781 GTGCTTTTCTGCTGCTTTTCCAGGAACACTTTGCTCCTGAGGATGAGAGAGAGCTAC 840
 DB 781 GTGCTTTTCTGCTGCTTTTCCAGGAACACTTTGCTCCTGAGGATGAGAGAGAGCTAC 840

QY 841 CACCTGGACGCAAGTGTTCAGGTCAACAGCTGGTAGCCACACCACTGCTGCTCAAC 900
 DB 841 CACCTGGACGCAAGTGTTCAGGTCAACAGCTGGTAGCCACACCACTGCTGCTCAAC 900
 QY 901 CGCTGCTCTTATTTGCTTCTTGACCGGAAGGCTTTATGAGATACCTTCGACGCTGTTT 960
 DB 901 CGCTGCTCTTATTTGCTTCTTGACCGGAAGGCTTTATGAGATACCTTCGACGCTGTTT 960
 QY 961 CCACGGTCAATGATATCCCTATCAAGTATGAGAGGCTTATCAGCAAGGCTCCAGG 1020
 DB 961 CCACGGTCAATGATATCCCTATCAAGTATGAGAGGCTTATCAGCAAGGCTCCAGG 1020
 QY 1021 GAAGTCTATGGCAGGCCCATTTGAACCTGACAGCAATTTGCATCAAGGCGAGGATATA 1080
 DB 1021 GAAGTCTATGGCAGGCCCATTTGAACCTGACAGCAATTTGCATCAAGGCGAGGATATA 1080
 QY 1081 TAA 1083
 DB 1081 TAA 1083
 RESULT 2
 ID ADO30354
 AC ADO30354 standard; cDNA; 1083 BP.
 XX ADO30354;
 XX 29-JUL-2004 (first entry)
 XX Mouse GPCR CMKBR1L2 polynucleotide, SEQ ID NO:1457.
 XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KW transgenic mouse; neurological disorder; adrenal gland disorder;
 KW colon disorder; intestinal disorder; cardiovascular disorder;
 KW muscular disorder; blood disorder; immune disorder; bone disorder;
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;
 KW kidney disorder; liver disorder; lung disorder; breast disorder;
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 KW thymus disorder; thyroid disorder; antiparkinsonian; antianemic;
 KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
 KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
 KW dermatological; antiulcer; antichryoid; antiallergic; anorectic;
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
 KW murine; gene; ss.
 XX Mus musculus.
 XX WO2004040000-A2.
 XX 13-MAY-2004.
 XX 09-SEP-2003; 2003WO-US028226.
 XX 09-SEP-2002; 2002US-0409303P.
 XX 09-APR-2003; 2003US-0461329P.
 XX (PRIM-) PRIMAL INC.
 XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
 XX Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;
 XX WPI; 2004-390329/36.
 XX P-PSDB; ADO29712.
 XX Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.
 XX Claim 151; SEQ ID NO 1457; 542pp; English.


```
/note= "Sequence flanking Neo insert in targetting
construct"
```

WO200203793-A2.

17-JAN-2002.

10-JUL-2001; 2001WO-US021923.

10-JUL-2000; 2000US-0217058P.

10-JUL-2000; 2000US-0217223P:

10-JUL-2000, 2000US-0217255P.
10-JUL-2000: 2000US-0217255P.

10-JUL-2000; 2000US-0217236P.
10-JUL-2000: 2000US-0217257P.

11-JUL-2000; 2000US=0217347P.
11-JUL-2000; 2000US=0217629P.

12-JUL-2000; 2000US-0217537P.
12-JUL-2000; 2000US-0219069P

12-JUL-2000; 2000US-0218074P.
12-JUL-2000; 2000US-0218075P.

27-JUL-2000; 2000US-0221483P.

07-AUG-2000; 2000US-0223122P.

15-NOV-2000; 2000US-0249408P.

16-JAN-2001; 2001US-0262113P.

[illegible]

P-PSDB; AAE20602.

Novel non-human transgenic and

gene. comprises disruptions i

Disclosure: Fig 15: 101pp: En

The invention relates to a no-

protein coupled receptor (GPCR)

gene, orphan GPR10 (UHR) -1) g

(EDG3) gene, ATP rece

expression or function

A transgenic construct

testing the effi-

psychotic illnesses. The transgenic animal is also useful as models for diseases, disorders or conditions associated with phenotypes relating to

drugs and interventions which may b

the expression of the target gene is useful as a therapeutic for treating conditions associated with a disruption of the target gene. The present sequence is mouse GPCR beta chemokine receptor (E01) gene

Sequence 2045 BP; 492 A; 509 C; 491 G; 553 T; 0 U; 0 Other;

99.4%; Score 1076.6; DB 6; Length 2045; every Match

Local Similarity 0.0, Mismatch: 0: Mismatch

1 ATGGATAACTACACAGTGGCCCCGGACGATGAATATGATGTCTTAATCTTAGACGACTAC 60

Db	445	ATGGATAACTACACAGTGGCCCCGGAGATATGATGTCTCTAATCTTTAGACGACTAC	504
Qy	61	CTGGACAACAGTGGGGCGGACCAAGTTCGGGCCCCGGAGTTCCTCTCCCCCGACAGGTG	120
Db	505	CTGGACAACAGTGGGGCGGACCAAGTTCGGGCCCCGGAGTTCCTCTCCCCCGACAGGTG	564
Qy	121	CTGCAGATTCTGTGCGGGGTGTTTGCGGTGGGTCTCTTGGAACAAGCTGTGCGGGTGT	180
Db	565	CTGCAGATTCTGTGCGGGGTGTTTGCGGTGGGTCTCTTGGAACAAGCTGTGCGGGTGT	624
Qy	181	ATCTTGCTGAAATACAAAGGACTCAAGAACTCGGGGAAACATCTACTTCTCTAAACCTGGCA	240
Db	625	ATCTTGCTGAAATACAAAGGACTCAAGAACTCGGGGAAACATCTACTTCTCTAAACCTGGCA	684
Qy	241	CTTTCAAACCTGTGTTTCTGCTTCCCTGCGGTCTTGCGGCCCATACTGACGACACAGGG	300
Db	685	CTTTCAAACCTGTGTTTCTGCTTCCCTGCGGTCTTGCGGCCCATACTGACGACACAGGG	744
Qy	301	GAAGCCCTCGCAACGGGACCTGTAAGTTCCTGTCGACTCCACTCTCGGCTTTATAC	360
Db	745	GAAGCCCTCGCAACGGGACCTGTAAGTTCCTGTCGACTCCACTCTCGGCTTTATAC	804
Qy	361	AGCGAGTGTGTTTCCAACTCCTCTCTGTGCAAGGATACAGGGTGTGTTTCCCAAGG	420
Db	805	AGCGAGTGTGTTTCCAACTCCTCTCTGTGCAAGGATACAGGGTGTGTTTCCCAAGG	864
Qy	421	CGAGTGGCTCCATCTTCAGACAGTGTCTGTGTGTTATGTTGCGGTGCATCTCGGCATGG	480
Db	865	CGAGTGGCTCCATCTTCAGACAGTGTCTGTGTGTTATGTTGCGGTGCATCTCGGCATGG	924
Qy	481	GCCATGCTACTGCGTCTCTTTGCCCGAGTCTGTGTGTTTATGAGCGCTCGEATGGAAGA	540
Db	925	GCCATGCTACTGCGTCTCTTTGCCCGAGTCTGTGTGTTTATGAGCGCTCGEATGGAAGA	984
Qy	541	CAGAAACAAAGTGTGCTTTGGGAAACCTCACTCTTGTGCAATCGAAGCGCGCTCTGG	600
Db	985	CAGAAACAAAGTGTGCTTTGGGAAACCTCACTCTTGTGCAATCGAAGCGCGCTCTGG	1044
Qy	601	AAGTACGTTCTGACGTCAAAAATGATCATCTGGTACTGTCTTTTCTCTGTGTTGTTT	660
Db	1045	AAGTACGTTCTGACGTCAAAAATGATCATCTGGTACTGTCTTTTCTCTGTGTTGTTT	1104
Qy	661	ATAATCTGCTCAGGCAACTGAGGAGAAGCAGAGCTTCAGGAGAGACAGTACGACCTC	720
Db	1105	ATAATCTGCTCAGGCAACTGAGGAGAAGCAGAGCTTCAGGAGAGACAGTACGACCTC	1164
Qy	721	CACAAGCCGCTCTGTGCATAAGCGGCGTGTCTCTTTTGATGTGGCGCCTTACACACT	780
Db	1165	CACAAGCCGCTCTGTGCATAAGCGGCGTGTCTCTTTTGATGTGGCGCCTTACACACT	1224
Qy	781	GTGCTTTTCGTCTGTCTTTCCAGGAACACTTGTCCCTGCAGGATGAGAAGACGCTAC	840
Db	1225	GTGCTTTTCGTCTGTCTTTCCAGGAACACTTGTCCCTGCAGGATGAGAAGACGCTAC	1284
Qy	841	CACCTGAGCGCAAGTGTTCAGGTCAACACGTGGTAGCGACCAACCACTGCTGGTCAAC	900
Db	1285	CACCTGAGCGCAAGTGTTCAGGTCAACACGTGGTAGCGACCAACCACTGCTGGTCAAC	1344
Qy	901	CCGCTGCTCTATTGCTTCTTGACCGGAAGCCCTTTATGAGATACCTTCGACGCTGTTTC	960
Db	1345	CCGCTGCTCTATTGCTTCTTGACCGGAAGCCCTTTATGAGATACCTTCGACGCTGTTTC	1404
Qy	961	CCACGCTGCAATGATATCCCTATCAAAAGTAGTGGAGGTATACGAAAGCGCTCCAAAG	1020
Db	1405	CCACGCTGCAATGATATCCCTATCAAAAGTAGTGGAGGTCTCAGCAAGCGCGCCAAAG	1464
Qy	1021	GAAGGTATCGCAGGCCCATTTGAACGTACAGCAATTTGCATCAAGGCAAGGATATAATA	1080
Db	1465	AAAGGTATCGCAGGCCCATTTGAACGTACAGCAATTTGCATCAAGGCAAGGATATAATA	1524
Qy	1081	TAA 1083	

Db	1525 TAA 1527	Best Local Similarity 65.2%; Pred. No. 5.8e-117; Matches 706; Conservative 5; Mismatches 338; Indels 33; Gaps 5;
RESULT 4		
ADQ38349		
ID	ADQ38349 standard; DNA; 1646 BP.	
XX		
AC	ADQ38349;	
XX		
DT	18-NOV-2004 (first entry)	
XX		
DE	Human SNP containing myocardial infarction-associated gene, SEQ ID 12.	
XX		
KW	Myocardial infarction; detection; single nucleotide polymorphism; SNP;	
KW	cardiac; gene therapy; human; gene; ds.	
XX		
OS	Homo sapiens.	
XX		
FN	WO2004058052-A2.	
XX		
PD	15-JUL-2004.	
XX		
XX	22-DEC-2003; 2003WO-US040978.	
XX		
PR	20-DEC-2002; 2002US-0434778P.	
PR	10-MAR-2003; 2003US-0453135P.	
PR	30-APR-2003; 2003US-0456412P.	
PR	23-SEP-2003; 2003US-0504955P.	
XX		
XX	(APPL-) APPLERA CORP.	
FA		
XX		
PI	Cargill M, Devlin JJ, Iakoubova O;	
XX		
XX	WPI; 2004-533949/51.	
DR	P-PSDB; ADQ38349.	
XX		
PT	Identifying an individual who has an altered risk for developing	
PT	myocardial infarction by detecting a single nucleotide polymorphism in	
PT	the individual's nucleic acids.	
XX		
XX	Claim 7; SEQ ID NO 12; 145pp; English.	
PS		
XX		
CC	The invention relates to a novel method for identifying an individual who	
CC	has an altered risk for developing myocardial infarction. The method	
CC	comprises detecting a single nucleotide polymorphism (SNP) in any one of	
CC	the nucleotide sequences given in the specification in the individual's	
CC	nucleic acids, where the presence of the SNP is correlated with an	
CC	altered risk for myocardial infarction in the individual. The invention	
CC	further comprises: an isolated nucleic acid molecule comprising at least	
CC	8 contiguous nucleotides where one of the nucleotides is an SNP given in	
CC	the specification or its complement and encoding any one of the amino	
CC	acid sequences given in the specification; an isolated polypeptide	
CC	comprising an amino acid sequence given in the specification; an antibody	
CC	that specifically binds to the polypeptide or its antigen-binding	
CC	fragment; an amplified polynucleotide containing an SNP given in the	
CC	specification and which is between about 16 and 1000 nucleotides in	
CC	length; a kit for detecting an SNP in a nucleic acid, comprising the	
CC	polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a	
CC	nucleic acid molecule; a method of detecting a variant polypeptide; and a	
CC	method for identifying an agent useful in treating or preventing	
CC	myocardial infarction. The novel detection method has cardiac activity.	
CC	The nucleic acids of the invention may be used in gene therapy. The	
CC	method is useful in identifying an individual who has an increased or	
CC	decreased risk for developing myocardial infarction and for preparing a	
CC	composition for treating or preventing myocardial infarction. This	
CC	polynucleotide sequence represents a human myocardial infarction-	
CC	associated gene containing one or more SNPs of the invention. Note: This	
CC	sequence was not shown in the specification. The sequence has come from	
CC	an electronic sequence listing downloaded from the WIPO website.	
XX		
XX	Sequence 1646 BP; 438 A; 381 C; 356 G; 459 T; 0 U; 12 Other;	
XX		
XX	Query Match 39.1%; Score 423.2; DB 13; Length 1646;	

QY	1	ATGGATAACTACAGTGGCCCGGACGATGAATATGATGCTCTTAATCTTAGACCACTAC	60
Db	202	ATGGCCAATTHCAGCTGGCCACGAGATGAATATGATGCTCTTAATCTTAGACCACTAC	258
QY	61	CTGGACAACAGTGGCCCGGACCAAGTT-----CGGCCCGCCGAGTTCTCTCTCCCGCAG	114
Db	259	CTGGAGAGCGATGAGGACGAGCAATGTGACAAGTATGAGCCCGGACCTCTCAGCCCGAG	318
QY	115	CAGTGTGTCAGTTCTGCTGCGCGGTGTTGCGGTGGGTCTCTTGGACAACGTCGTGGCG	174
Db	319	CTGGTGGCCATCACTCTGCTCTGCTGTTGTTGATGCGGTGCTCTGGACAATCTCTCGTT	378
QY	175	GTGTTTATCTTGGTGAATACAAAGGACTCAAGAAATCTGGGGAAACATCTACTTCTTAAC	234
Db	379	GTGCTTATCTCTGGTAAATATATAAGGACTCAACCGGTGGAAATATCTATCTTCTTAAC	438
QY	235	CTGGCACTTTCAAACTGTGTTCTCTGCTCCCTGCGGTTCTGGGCCCATATCTGACGA	294
Db	439	TGGCAGTTTCTAACTTGTGTTCTTGTCTTACCTGCGCTTCTGGGCTCATGCTG-----	493
QY	295	CACGGGAAACCCCTGCAACGGGACCTGTAAAGTTCTTGTGGACTCACTCTCTCGGC	354
Db	494	-----RKGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGCGGC	540
QY	355	TTATACAGCGAGTGTGTTTCCCAACATCTCTCTCTGTGCAAGGATACAGGGTGTGTTCC	414
Db	541	CTGTACAGTGAGACATTTTCAATGCTTCTGACTGTGCAAGGATCTAGTGTGTTTG	600
QY	415	CAAGGCGAC---TGGCCTCCATCTTACGACAGTGTCTTGTGTTATTTGTTGCGTCATC	471
Db	601	CACAAGGGMAACTTTTCTCAGCCAGGAGGGTGCCTCTGCGCATCATTTACAGTGTCT	660
QY	472	CTGCGATGGGCACTGGCTATCTGCGCTCTCTTTGCGGAGTCTGTGTTTATGAGCTCGG	531
Db	661	CTGCGATGGGTAAACAGCCATTTCTGCGCACTTTGCGCTGAATTCRTGTTTATAAACCTCAG	720
QY	532	ATGGAAGACAGAACACAAAGTGTGCTTTGGCAAACTCACTCTTCTGCCAATCGAAGCG	591
Db	721	ATGGAAGACCAAGAAATACAAAGTGTGCAATTTAGCAGAACTCCCTCTCCTCCAGTGTAG	780
QY	592	CCGCTCTGGAAGTACGTTCTGACGCTCAAAATATGATCATCTTGTGTAATTTCTCTCTG	651
Db	781	ACATTTCTGGAAGCATTTTCTGACTTTAAATGAACATTTTGGTTCTTGTCTCTCCCTA	840
QY	652	CTGTTTTTATATCTCTGCTGAGGCACTGAGGAGAGGAGAGCTTCAGGAGAGACAG	711
Db	841	TTTATTTTATCATTTCTTATGTGCAAAATGAGAAAAACACTTAAGGTTTCAGGAGAGAGG	900
QY	712	TACGACCTCCACAGCGGCTTTGTGCTAATACGGGCGTTCCTTTTGTATGTTGGCGCT	771
Db	901	TATAGCTTTTCAAGCTGTTTGTGCTTATGTTAGTGTCTTCTCTCTGATGTTGGCGCC	960
QY	772	TACAACACTGTGCTTTTCTGCTCTGCTTTCAGGAACACTTGTCTCTCGAGGATGAGAAG	831
Db	961	TACAATATGCAATTTTCTCTGCTCCTTTCAAAGAACACTTCTCCTGAGTGTGCAAG	1020
QY	832	AGAGCTTACCACTTGGAGCGAAGTGTTCAGGTCAACAGCTGTGAGGACCACTCTGTC	891
Db	1021	AGCAGCTTACAATCTGGACAAAAAGTGTTCACATCACTAAACTCATCGCCACCACTGTC	1080
QY	892	TGCTTCAACCGCTGCTCTATTTGCTTCTTGGCCGAGGCGCTTTTATGAGATACCTTCGC	951
Db	1081	TGCATCAACCTCTCTCTGATGCGTTTCTTGTATGCGA---CATTTAGCAATATCTCTGC	1137
QY	952	AGCCTGTTCCCAACGGTGAATGATATCCCTCTATCAAAAGTAGTGGAGGCTATCAGCAAGCG	1011
Db	1138	CGCTGTTTCCATCTGCGGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACAAGGC	1197
QY	1012	CTTCAAGGAGGTGTCATGGCAGGCCCATTTGAACTGTACAGCAATTTGCAATCAAGGCGAG	1071

Db 1198 ACATCGAGGAGAACCTGACCATTCACCGAAGTGTAACATAGCATCCACCAATGCAA 1257

Qy 1072 GA 1073

Db 1258 GA 1259

RESULT 5

ADQ38350 standard; DNA; 1776 BP.

AC AC

DT 16-NOV-2004 (first entry)

XX Human SNP containing myocardial infarction-associated gene, SEQ ID 13.

DE Myocardial infarction; detection; single nucleotide polymorphism; SNP;

KW cardiant; gene therapy; human; gene; ds.

XX Homo sapiens.

OS WO2004058052-A2.

XX 15-JUL-2004.

XX 22-DEC-2003; 2003WO-US040978.

XX 20-DEC-2002; 2002US-0434778P.

PR 10-MAR-2003; 2003US-0453135P.

PR 30-APR-2003; 2003US-0466412P.

PR 23-SEP-2003; 2003US-0504955P.

XX (APPL-) APPLERA CORP.

PA Cargill M, Devlin JJ, Iakoubova O;

XX WPI; 2004-533949/51.

XX P-PSDB; ADQ39178.

XX Identifying an individual who has an altered risk for developing

PT myocardial infarction by detecting a single nucleotide polymorphism in

PT the individual's nucleic acids.

XX Claim 7; SEQ ID NO 13; 145pp; English.

XX The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiac activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.

Db 1264 CGCTGTTCCATCTCGGTAGTAACACCCCACTTCAACCCAGGGGCGAGTGTGCACAAAGGC 1323
 Qy 1012 CCTCAAGGGAGGTCTAGGAGGCCCATTTGAACGTATACAGCAATTTGCATCAAGGCAG 1071
 Db 1324 ACATCGAGGGAAGAACCTGACCACTTCCACCAAGGTGTAACTAGCATCCACCAATGCAA 1383
 Qy 1072 GA 1073
 Db 1384 GA 1385

RESULT 6

ACH89585
 ID ACH89585 standard; DNA; 1140 BP.

XX ACH89585;

DT 29-JUL-2004 (first entry)

XX Human genome derived single exon probe #22780.

XX Human; probe; ss; gene expression; single exon probe; microarray;
 alternative splicing event; genomic alteration.

XX Homo sapiens.

XX US2003194704-A1.

XX 16-OCT-2003.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX (PENN/) PENN S G.

XX (HANK/) HANK D R.

XX (HANZ/) HANZEL D K.

XX Penn SG, Rank DR, Hanzel DK;
 WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human
 gene expression analysis, for identifying or characterizing alternative
 splicing events, for assessing genomic alterations or as tools for
 surveying tissues.

XX Claim 1; SEQ ID NO 22780; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene
 expression, comprising any of the 27,400 fully defined nucleotide
 sequences in the specification, or their complements or fragments, and
 encoding at least 8 amino acids of any of the 688 amino acid sequences
 fully defined in the specification. The probe is a single exon probe that
 hybridises under high stringency conditions to a nucleic acid molecule
 expressed in human cells or tissues. Also included are a spatially-
 addressable set of single exon nucleic acid probes for measuring human
 gene expression (comprising a plurality of single exon nucleic acid
 probes cited above, where each of the plurality of probes is separately
 and addressably isolatable or amplifiable from the plurality), a single
 exon microarray for measuring human gene expression, a method of
 measuring human gene expression, a vector comprising the single exon
 probe cited above, an ORF-encoded peptide comprising at least 8
 contiguous amino acids of any of the above-mentioned amino acid
 sequences (optionally with conservative amino acid substitutions), an
 isolated antibody that binds specifically to a peptide cited above,
 methods of selling and/or licensing single exon probes or microarrays to
 a customer desiring to measure gene expression, a method of providing
 human gene expression data by subscription, and a computer-readable
 storage medium which contains a database having a plurality of records
 (each record including data on the expression of a single exon probe
 cited above). The probe, methods and apparatus are useful in gene
 expression analysis. The probe may be used as tools for surveying

CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterising
 CC alternative splicing events, in detecting and characterising gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704
 XX

SQ Sequence 1140 BP; 294 A; 275 C; 241 G; 330 T; 0 U; 0 Other;

Query Match 39.0%; Score 422; DB 12; Length 1140;

Best Local Similarity 65.5%; Pred. No. 1.1e-116; Indels 33; Gaps 5;

Matches 709; Conservative 0; Mismatches 340;

Qy 1 ATGGATAAATACTACACAGTGGCCCCCGGACGATGAATATGATGTCCTTAATCTTAGACGACTAC 60
 Db 13 ATGGCCAATTTACACGCTGGCACCAGAGGATGATATGATGTCC--TCATAGAAGGTGAA 69
 Qy 61 CTGGACAACAGTGGCCCGGACCAAGTT-----CCGGCCCCCGAGTTCCTCTCCCCCAG 114
 Db 70 CTGGAGAGCGATGAGGCAGAGCAATGTGACAAGTATGACGCCCGGCACTCTCAGCCAG 129
 Qy 115 CAGGTGTCGCAAGTTCCTGTCGGCGGTGTTGCGGTGGTCTCTTGGACAAGCTGCTGGCG 174
 Db 130 CTGCTGCATCACTCTGCTCTGCTGTTGTTGATCGTGTCTCTGGACATCTCTCTGTT 189
 Qy 175 GTGTTTATCTTGGTGAATAACAAGGACTCAAGAACTCTGGGGAACATCTACTTCTTAAAC 234
 Db 190 GTGCTTATCTCTGGTAAATAATAAAGGACTCAACCGCTGGAAATAATCTATCTTCTTAAAC 249
 Qy 235 CTGGCACTTTCAAACTGTTTCTGCTGCTCCCTCGCGGTTCGGGCCCACTACTGCAGCA 294
 Db 250 TTGGCAGTTTCTAACTTGTGTTCTTGTCTTACCTTCCCTTCTGGGCTCATGCTG----- 304
 Qy 295 CACGGGGAAGCCCTGGCAACGGGACCTGTAAAGTCTTGTGCGGACTCCACTCTCTGGGC 354
 Db 305 -----GGGCGGATCCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGTGGGC 351
 Qy 355 TTATACAGCGAGGTGTTTTTCCAAACATCTCTCTCTTGTGCAAGGATACAGGGTGTTC 414
 Db 352 CTGTACAGTGAGACATTTTTTCAATTGCTTCTGACTGTGCAAAAGGTACCTAGTGTGTTTG 411
 Qy 415 CAAGGGCGAC---TGGCTCCTATCTTCACAGAGTGTCTGTGTGATATGTTGCGTGATC 471
 Db 412 CACAAGGGCAACTTTTTTCTCAGCCAGGAGGGTGCCTGTGGCATCATTTACAAAGTGT 471
 Qy 472 CTGSCATGGGCCCATGGCTACTGCGCTCTCTTTGGCCGAGTCTGTGTTTATGAGCCTCGG 531
 Db 472 CTGSCATGGGTACAGCCATTTCTGGCCACTTTGCTGTAATACGTGGTGTATTAACCTCAG 531
 Qy 532 ATGGAAGACAGAAACAACAGTGTGCTTTTGGCAAACTCCTCTTTGCCAATCGAAGCG 591
 Db 532 ATGGAAGACCAGAAATACAAAGTGTGCATTTTAGCAGAACTCCCTTCTGCCAGCTGATGAG 591
 Qy 592 CCCTCTGGAAGTACGTCTTCAGCTCAAAAATGATCATCTTGTGACTCTTTTCTCTCTG 651
 Db 592 ACATTCTGGAAGCATTTTCTGACTTTTAAAAATGAACAATTTGCGGTCTTGTCTCTCCCTA 651
 Qy 652 CTGTTTATTAATATCTGCTGACGCAACTCAGGAGAGGAGGAGAGCTTTCAGGAGAGAGCAG 711
 Db 652 TTTATTTTACATTTCTATGTGCAATGAGAAAAAACAATAAGTTTCAGGAGAGAGAGG 711
 Qy 712 TAGCACTCCACAAGCGCGCTCTTGTCTAATACCGGCGTGTTCCTTTTGTATGTGGCGCCT 771
 Db 712 TATAGCTTTTCAAGCTGTTGTTTTTGGCATAATGAGTAGTCTTCTTCTGATGTGGCGGCC 771
 Qy 772 TACAACACTGTGCTTTTCTGCTGTCTTCCAGGAACACTTGTCCCTGCGAGGATGAGAG 831
 Db 772 TACAATATTGCATTTTCTTCTGCTGCTCACTTTTCAAAAGAACACTTCTCCCTGAGTGACTGCAAG 831

QY 832 AGCAGCTACCACTGGAGCGAAGTTTCAGGTACACAGCTGGTATGGACCAACCACTGC 891
DB 832 AGCAGCTACCACTGGAGCGAAGTTTCAGGTACACAGCTGGTATGGACCAACCACTGC 891
QY 892 TGGCTCAACCCGCTGCTCTATTGCTTCTTGACCGGAAGCCCTTATGAGATACCTTCGC 951
DB 892 TGGCTCAACCCGCTGCTCTATTGCTTCTTGACCGGAAGCCCTTATGAGATACCTTCGC 948
QY 952 AGCTGTTCCTCCAGCGTGCATATATCCCTATCAAAAGTATGAGGCTATCAGCAAGCG 1011
DB 949 CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGGGAGTCTGCACAAGGC 1008
QY 1012 CTCTCCAGGGAAGTATGCGAGCCCATTTGAATCTGACAGCAATTTGCAATCAAGGCAG 1071
DB 1009 ACATCAGGGAAGAACCTGACCATTTCCACCGAAGTGTAAACTAGCATCCACCAATGCAG 1068
QY 1072 GA 1073
DB 1069 GA 1070

RESULT 7
ID ABL88079 standard; cDNA; 1475 BP.
XX ABL88079;
AC ABL88079;
XX
XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO1873 cDNA sequence SEQ ID NO:15.
XX
XX Human; angiogenesis; cardiast; cytostatic; antiangiogenic; hypotensive;
KW vulnary; antarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping; gene; ss.
XX
OS Homo sapiens.
XX
XX WO200200690-A2.
XX
XX 03-JAN-2002.
XX
XX 20-JUN-2001; 2001WO-US019692.
PF
XX
PR 23-JUN-2000; 2000US-0213637P.
PR 20-JUL-2000; 2000US-0219556P.
PR 23-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00702328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 01-MAR-2001; 2001WO-US006520.
PR 09-MAR-2001; 2001US-00802706.

PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 25-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
XX
PA (GETH) GENENTECH INC.
XX
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
DR P-PSDB; ABB84824.
DR
DR WPI; 2002-090516/12.
XX
XX
PS Claim 2; Fig 15; 565pp; English.
XX
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC antiangiogenic, hypotensive, vulnary and antarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The PRO polynucleotides have applications in molecular biology,
CC including use as hybridisation probes, and in chromosome and gene
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC exemplification of the present invention
XX
SQ Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;
Query Match 39.0%; Score 422; DB 6; Length 1475;
Best Local Similarity 65.5%; Pred. No. 1.3e-116;
Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;
QY 1 ATGGATAACTACACAGTGGCGCCCGGACGATGATATGATGCTCTTAATCTTAGACGACTAC 60
DB 29 ATGGCCAATTACACGCTGGCACGACGAGGATGATATGATGCTCC---TCATAGAAGGTGAA 85
QY 61 CTGGACAAACAGTGGCGCGGACCAAGTT-----CGGCGCCCGGAGTTCCTCTCCCCCAG 114
DB 86 CTGGAGAGCGATGAGGCGAGCAAGTCTGACAAAGTATGACGCCCGGACGACTCTCAGCCAG 145
QY 115 CAGGTGCTGCAGTTCCTGCTGGCGGTGTTTGGGTGCTCTTGGACACGCTGGCGG 174
DB 146 CTGGTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 205
QY 175 GTGTTTATCTTGGTGAATAACAAGGACCAAGAACTCGGGGAACATCTATCTCTTAAC 234
DB 206 GTGCTTATCTGTTAAATAATAAAGGACCAACGCGTGGAAATAATCTATCTCTTAAC 265
QY 235 CTGGCACTTTCAAACTGTGTTTCTGCTTCCCTGCGGTTCCTGGGCCCATCTATCGAGCA 294
DB 266 TTGGCAGTTTCTAACTGTGTTTCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 320
QY 295 CACGGGGAAAGCCCTGCGCAACGGGACCTGTAAAGTTCCTTGTGGAGCTCCCACTCTCGGGC 354
DB 321 -----GGGGCGATCCCATGTGTAAATTTCTCATGTGACTTCTGCTGGGC 367
QY 355 TTATACAGCGAGGTGTTTTCACATCTCTCTCTTGTGCAAGGATACAGGGGTGTTTTC 414

CC	angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC	angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC	healing. The present sequence is a coding sequence of the invention
XX	
SQ	Sequence 1475 Bp; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;
	Query Match 39.0%; Score 422; DB 6; Length 1475;
	Best Local Similarity 65.5%; Pred. No. 1.3e-116;
	Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5
Qy	1 ATGGATAACTACACAGTGGCCCCGGACGATGAATATGATGTCCTAATCTTAGACGACTAC 60
Db	
29	ATGGCCAAATTACACGCTGGCACGAGGATGAATATGATGTC---TCATAGAAGGTCAA 85
Qy	61 CTGGACAACAGTGGCGCGGACCAAGTT-----CGGCCCCCGAGTTCCTCTCCCCCCAG 114
Db	
86	CTGGAGAGCGATGAGGAGAGCAATGTGACAAGTATGACGCCGAGGCACTCTCAGCCCCAG 145
Qy	115 CAGGTGCTGCAGTTCTGCTGCGCGGTGTTTCGGGTGGGTCTCTGGACAACGTCGTGGCG 171
Db	
146	CTGGTGCATCACTCTGCTCTGCTGTTGTGTGATCGGTGTCCTGGACAATCTCTGGTT 205
Qy	175 GTGTTTATCTTGGTGAATACAAGGACTCAAGAAATCTGGGGAACATCTACTTCTTAAC 234
Db	
206	GTGCTTATCTGGTAAATAATAAGGACTCAAAACGCGTGGAAAAATATCTATCTCTTAAC 265
Qy	235 CTGGCACTTTCAAACTGTGTTTCTGCTCCCTGCCGTCTCGGCCCATACTGCAGCA 294
Db	
266	TTGGCAGTTTCTAACTTGTGTTTCTTGCTTACCCTGCCCTCTCGGCTCATGCTG----- 320
Qy	295 CACGGGAAAGCCCTGGCAACGGGACCTGTAAAGTTCTTGTGGAACCTCACTCTCGGGC 354
Db	
321	-----GGGGCATCCCATGTGTAATAATCTCATTTGGACTGTACTTCTGTGGGC 367
Qy	355 TTATACAGCAGGTGTTTTTCCAAATCTCTCTCTTGTGCAAGGATACAGGGTGTCTTC 414
Db	
368	CTGTACAGTGAACAATTTTTCAATTTGCCCTCTGACTGTGCAAAAGGTACTATGTTGTTG 427
Qy	415 CAAGGGCGAC---TGCGCTCCATCTTACGACAGTGTCTTGTGTTATGTTTGGTGCATC 471
Db	
428	CACAAGGGCACTTTTTCTAGCAGAGGAGGGTGCCTGTGGCATCATTTACAAGTGC 487
Qy	472 CTGCGATGGGCCATGGCTATCGCGCTCTCTTTTGGCCGAGTCTGTGTTTTATGAGCCTCG 531
Db	
488	CTGCGATGGGTAAACAGCCATTTCTGGCCACTTTTGCCTGAATACGTGGTTTATAAAACCTCAG 547
Qy	532 ATGAAAGACAGAAACAAGTGTGCCTTTCGCAAAACCTCACTTCTGSCCAATCGAAGCG 591
Db	
548	ATGGAAGACCGAAATACAGTGTGCATTTAGCAGAACCTCCCTCTCTGCCAGTGTATGAG 607
Qy	592 CCGCTCTGGAGTAGTCTTGACGCTCAAAAATGATCATCTTGGTATCTTGCTTTTCTCTG 651
Db	
608	ACAATCTGGAAGCATTTTCTGACTTTAAAAATGAACATTTTCGGTTCCTTGCTCCCCCTTA 667
Qy	652 CTGTTTTTTTATAATCTGCTCAGGCAACTGAGGAGAGGAGAGGCTTCAGGGAGAGACAG 711
Db	
668	TTTTATTTTACATTTCTATATGTCAATATGAAAAACAATAAGGTTTCAGGGAGCAGAGG 727
Qy	712 TACGACCTCCAAGCGGGCTTGTGTATACGGCGGTGTTTCTTTTATGATGGCGCGCT 771
Db	
728	TATAGCCTTTTCAAGCTTGTTTTTGCCAATATGTTAGTCTTCTTCTGATTTGGGGGCC 787
Qy	772 TACAACATCTGTGCTTCTGCTCTTTCAGGAACAATTGTGCCCTCAGAGATGAGAAG 831
Db	
788	TACAATATTGATTTTTTCTGTCCAATTTCAAAGAAACACTTCTCCCTGAGTGACTGTCAAG 847
Qy	832 AGCAGCTACCACTTGGACGCAAGTGTTCAGGCTCACAGCTGGTAGCGACCAACCACATGC 891
Db	
848	AGCAGCTACAAATCTGGACAAAGTGTTCACATCACTAAACTCATCGCCACCAACCACATGC 907
Qy	892 TGGCTCAACCCGCTGCTCTATTTTGGTCTTTCAGCCGGAAGGCGCTTATGAGATACCTTCG 951
Db	
908	TGCATCAACCTCTCTCTGTATGCGTTTCTGATGGGA---CATTTAGCAATATCTCTGCG 964

cell tube formation. The present sequence represents a cDNA encoding a PRO polypeptide of the invention.

Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;

Query Match 39.0%; Score 422; DB 10; Length 1475;

Best Local Similarity 65.5%; Pred. No. 1.3e-116;

Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;

```
CC 1 ATGGATACTACAGTGGCCGCGGACGATGAATATGATGCTTAATCTTAGACGACTAC 60
CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 29 ATGGCAATTACACCTGGCACCAGAGGATGAATATGATGCTTCTTCCATGAAGGTGAA 85
SQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 CTGGACAACAGTGGCCGCGGACCAAGTT-----CGGCCCCCGAGTCTCTCTCCCCCAG 114
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 86 CTGGAGCGGATGAGCGAGAGCAATGTGCAAGTATGACGCCCGGACACTCTCAGCCAG 145
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 115 CAGTGTCTGAGTCTCTGTCGGCGGTGTTTGGGGTCTCTTGGACAACAGTGTCTGGCG 174
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 146 CTGGTGCATCACTCTGCTCTGCTGTTTGTGATCGGTGCTCTGGACAATCTCTCTGTT 205
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 175 GTGTTTATCTTGTGAATACAAAGCACTCAAGATCTGGGNAACATCTACTTCTTAAC 234
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 206 GTGCTTATCTTGTGAATATAAAGGACTCAACCGGTGGAATAATCTATCTTCTAAAC 265
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 235 CTGGCACCTTTCAAACCTGTGTTTCTGCTTCCCTGCGGTTCTGGGCCCATCTGCGAGCA 294
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 266 TTGGCAGTTTCTAACTGTGTTTCTGTTTACCTGCGCTTCTGGGCTCATGCTG----- 320
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 295 CACGGGGAAGCCCTGGCAACGGGACCTGTAAAGTTTCTTGTGCGACTCCATCTCTCGGGC 354
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 321 -----GGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGTGGC 367
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 355 TTATACGCGAGGTGTTTCCAAATCTCTCTCTCTGTCAGAGGATACAGAGTGTCTTCC 414
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 368 CTGTACAGTGAGACAATTTTCAATTGCGCTTCTGACTGTGCAAGGTACTAGTGTGTTTG 427
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 415 CAAGGGCCGAC---TGGCCTCCATCTTACGACAGTGTCTTGTGTTATGTTGCGTGCATC 471
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 428 CACAAGGCACTTTTCTGACGCGAGGAGGAGTGGCTGTGGCATCATTTACAAGTGTG 487
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 472 CTGGCATGGGCGCATGGCTACTGCGCTCTCTTGGCCGAGTCTGTGTTTATGAGCCTCGG 531
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 488 CTGGCATGGGTAAACAGCACTTCTGGCCACTTTCCTGTAATACGTGTTTATAAACCTCAG 547
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 532 ATGGAAGACAGAAACACAGTGTGCTTTCGCAACCTCACTCTTGGCAATCGNAGCG 591
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 548 ATGGAAGACCAAGAAATACAAGTGTGCAATTTAGCAGAACTCCCTTCTGCGAGCTGATGAG 607
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 592 CCGCTCTGGAAGTACGTTCTGACGTCACAAAATGATCATCTTGTGTTTCTCTCTG 651
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 608 ACATCTGGAAGCATTTTCTGACTTAAATATGAACATTTGCTTCTCTCTCTG 667
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 652 CTGTTTTTATAATCTGCTGAGCAACTGAGGAGGAGGAGCTTCAAGGAGAGACAG 711
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 668 TTTATTTTACATTTCTATGTGCAATGAGAAAACACTAAGGTTTCAGGAGCAGAGG 727
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 712 TACGACTCCCAAGCGGCTTGTGATACAGGCGGTGTTCTTGTATGTTGGCGCT 771
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 728 TATAGCTTTTCAAGCTGTTTGTGCCATATGATGATGTTCTTCTGATGTTGGCGGCC 787
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 772 TACAACACTGTGCTTCTGCTGCTTTCAGGAACACTTGTCCCTGCGAGTGAAGAG 831
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 788 TACATATTTGATTTTCTGCTTCACTTTCAAGAACACTTCTCCTGAGTGAAGAG 847
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 832 AGCAGTACCACTGGAGCGCAAGTGTTCAGTCTACAGCTGTGAGCAACCCACTGCG 891
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 848 AGCAGTACAATCTGGAACAAAGTGTTCACATCACTAACTCATCGCCACCACTGCG 907
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 892 TGGCTCAACCGCTGCTCTATTGTTTCTTACCGGAGGCTTTATGAGATACCTTGGC 951
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 908 TGCATCAACCCCTCTCTGCTGATGCGCTTCTGATGGGA---CATTTAGCAATACCTCTGC 964
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 952 AGCTGTTTCCACCGTGAATGATATCCCTATCAAACTAGTGGAGGCTATCAGCAAGC 1011
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 965 CGCTGTTTCCATCTGCGTAGTAACACCCACTTCAACCAGGGGCGAGTCTGCACAGGC 1024
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1012 CCTCAAAGGAAGTCAATGCGCAGGCCCATTTGAACCTGTACAGCAATTTTCATCAAAAGGCAG 1071
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1025 ACATCGAGGGAAGAACCTGACCATTTCCACCGAAGTGTAAACTAGCATCCCAATGCA 1084
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1072 GA 1073
DB |||||
QY 1085 GA 1086
DB |||||

RESULT 10
ADD11264
ID ADD11264 standard; cDNA; 1475 BP.
XX
AC ADD11264;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human secreted/transmembrane PRO polypeptide cDNA #8.
XX
KW ss; gene; human; secreted protein; transmembrane protein;
cardiovascular disorder; endothelial disorder; angiogenic disorder;
myocardial infarction; cardiac hypertrophy; trauma; cancer;
age-related macular degeneration; angiogenesis;
endothelial cell apoptosis; smooth muscle cell growth;
endothelial cell tube formation.
XX
OS Homo sapiens.
XX
PN US2003105013-A1.
XX
PD 05-JUN-2003.
XX
PF 16-AUG-2002; 2002US-00223090.
XX
PR 20-JUN-2001; 2001WO-US019692.
PR 09-JUL-2001; 2001WO-US021735.
PR 20-FEB-2002; 2002US-00081056.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
Watanabe CK, Williams PM, Wood WI, Ye W;
XX
WPI; 2003-801242/75.
P-PSDB; ADD11265.
XX
New isolated nucleic acid encoding a secreted and transmembrane
polypeptide, useful for treating a cardiovascular, endothelial, or
angiogenic disorder in a mammal, such as cancer or age-related macular
degeneration.
XX
Claim 2; SEQ ID NO 15; 493pp; English.
XX
The invention relates to an isolated nucleic acid encoding a secreted and
transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
by the nucleic acid, or an agonist or antagonist, is used to treat a
cardiovascular, endothelial, or angiogenic disorder in a mammal,
preferably a human. The human may have suffered a myocardial infarction
or has cardiac hypertrophy, trauma, a cancer, or age-related macular
degeneration. The cardiac hypertrophy is characterized by the presence of
an elevated level of PGF-2 alpha. A PRO polypeptide, given in the
specification, or an agonist is used to inhibit or stimulate endothelial
cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
polypeptide, given in the specification, or an agonist is used to
stimulate or inhibit smooth muscle cell growth, or to induce endothelial
cell tube formation. The present sequence represents a cDNA encoding a
```


XX	Sequence	1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;
SQ	Query Match	39.0%; Score 422; DB 10; Length 1475;
	Best Local Similarity	65.5%; Pred. No. 1.3e-116;
	Matches	709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;
Qy	1	ATGGCAATTAACAGTGGCCCGGACGATGAATATATGATGCTTAATCTTAGAGACTAC 60
Db	29	ATGGCAATTAACAGTGGCCCGGACGATGAATATATGATGCTTAATCTTAGAGACTAC 85
Qy	61	CTGGACAACAGTGGCCCGGACGATGAATATATGATGCTTAATCTTAGAGACTAC 114
Db	86	CTGGACAACAGTGGCCCGGACGATGAATATATGATGCTTAATCTTAGAGACTAC 145
Qy	115	CAGGTCTGCGAGTCTGCTGCGCGGTGTTTGGGTGGGTCTTGGGACAAAGTGTCTGGCG 174
Db	146	CTGTTGCCATCAGTCTGCTGCTGCTGTTGTGATCGGTGCTGGACAACTCTCTGTT 205
Qy	175	TGTTTTATCTTTGGTGAATACAAAGGACTCAAGAACTCTGGGAAACATCTACTTCTTAAC 234
Db	206	GTGCTTATCTCTGTTAAATATAAAGGACTCAAGCGGTGGAAATATCTATCTTCTTAAC 265
Qy	235	CTGGCACTTTCAACCTGTTTCTGCTTCCCTGCGGTTCTGGGCCCACTACTGCAGCA 294
Db	266	TGGCAGTTTCTAACTTGTGTTCTGCTTACCCTGCGGCTTCTGGGCTCATGCTG----- 320
Qy	295	CACGGGAAAGCCCTGGCAACGGGACCTGTAAGTTCTTGTGGACTCCACTCTCGGGC 354
Db	321	-----GGGGCGATCCCATGTGTAAATCTCATTTGAGCTACTCTGTGGC 367
Qy	355	TTATACAGCGAGTGTGTTTCAACATCTCTCTCTGTGCAAGGATACAGGGTGTGTTTC 414
Db	368	CTGTACAGTGAGACATTTTCAATGTCCTCTGACTGTGCAAGGACTACTAGTGTGTTTG 427
Qy	415	CAAGGGCAGC---TGGCTTCATCTTACGACAGTGTCTTGTGTTATGTTGGTGCATC 471
Db	428	CACAAGGGCAACTTTTCTACGCCAGGAGGAGGCTGCGCTGTGGCATCAITACAAAGTGC 487
Qy	472	CTGCGATGGGCGATGGCTTACTGCTCTCTTGGCCGAGTCTGTGTTTATGAGCCTCGG 531
Db	488	CTGCGATGGGTAACAGCACTTCTGCGCACTTGTGCTGTAATACGTGGTGTATTAACCTCAG 547
Qy	532	ATGGAAGACAGAAACACAAAGTGTGCTTTTGGCAAACTCTCACTTCTTGCCAAATCGAAGCG 591
Db	548	ATGGAAGACAGAAATACAAGTGTGCAITTAGCAGAACTCTCTTCTGCGCAGCTGATGAG 607
Qy	592	CCGCTCTGGAAGTACGTTCTGACGTCAAAATGATCATCTTGGTACTGCTTTTCTCTCTG 651
Db	608	ACATTCTGGAAGCATTTTCTGACTTTAAATAATGAACATTTTGGTCTTCTCTCTCTCTG 667
Qy	652	CTGCTTTTATAATCTGCTGAGGCACTGAGGAGGAGGAGCTTCAGGGAGAGACAG 711
Db	668	TTTATTTTATCATTTCTATGTGCAATGAGAAACACTAAGTTTCAGGGAGCAGAGG 727
Qy	712	TACGACCTCCAAAGCGGCTCTTGTATACAGCGGCTGTTCTCTTTGATGTGGCGCCT 771
Db	728	TATAGCTTTTCAAGCTTGTGTTGGCAATATGATGCTTCTCTGATGTGGCGGCC 787
Qy	772	TACAACACTGTGCTTTTCTGCTGCTTTTTCAGGAAACACTTGTCCCTGCGAGGATGAGAG 831
Db	788	TACAATATTCATTTTCTGCTGCACTTTTCAAGAAACACTTCTCCCTGAGTGACTGCAAG 847
Qy	832	AGCAGCTACCACTGAGCGAAGTGTTCAGTCTACAGCTGTGAGGACCACTCCCTGCG 891
Db	848	AGCAGCTACCACTGAGCAAAAGTGTTCATCACTACTAACTCATCGCCACCACTCTGC 907
Qy	892	TGCGTCAACCGCTGCTCTATTTGCTCTTTCAGCGAAGGCTTTTATGAGATACCTTCGC 951
Db	908	TGCATCAACCTCTCTGCTGATGCTTCTTGTATGCGA---CATTTAGCAATACCTCTGC 964
Qy	952	AGCTGTTTCCCAACGGTGAATGATATCCCTTATCAAAAGTGTGAGGCTATCAGCAAGCG 1011

Db	965	CGCTGTTTTCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTTGCAACAAGGC 1024
Qy	1012	CTTCAAGGGAAGGTCTATGCGAGCCCGCATTTGAATGTACAGCAATTTGCATCAAGGCAG 1071
Db	1025	ACATCGAGGGAAGAACCTTGACCATTCACCGAAGTGTAACTAGCATCCCAAAATGCAA 1084
Qy	1072	GA 1073
Db	1085	GA 1086
RESULT 12		
ADE41265		
ID	ADE41265	standard; cDNA; 1475 BP.
XX		
AC	ADE41265;	
XX		
DT	29-JAN-2004	(first entry)
XX		
DE		Human secreted/transmembrane PRO polypeptide cDNA #8.
XX		
KW		ss: gene; human; secreted protein; transmembrane protein;
KW		cardiovascular disorder; endothelial disorder; angiogenic disorder;
KW		myocardial infarction; cardiac hypertrophy; trauma; cancer;
KW		age-related macular degeneration; angiogenesis;
KW		endothelial cell apoptosis; smooth muscle cell growth;
KW		endothelial cell tube formation.
OS		Homo sapiens.
XX		
PN	US2003100497-A1.	
XX		
PD	29-MAY-2003.	
XX		
PF	16-AUG-2002; 2002US-00223085.	
XX		
PR	20-JUN-2001; 2001WO-US019692.	
PR	09-JUL-2001; 2001WO-US021735.	
PR	20-FEB-2002; 2002US-00081056.	
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;	
PI	Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;	
PI	Watanabe CK, Williams PM, Wood WI, Ye W;	
XX		
DR	WPI; 2004-008957/01.	
XX		
XX	P-PSDB; ADE41266.	
PT		New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO205 or
PT		PRO214, useful in molecular biology, chromosome and gene mapping, in
PT		generating antisense RNA and DNA, and for treating disorders involving
PT		angiogenesis.
XX		
PS	Claim 2; SEQ ID NO 15; 492pp; English.	
XX		
CC		The invention relates to an isolated nucleic acid encoding a secreted and
CC		transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
CC		by the nucleic acid, or an agonist or antagonist, is used to treat a
CC		cardiovascular, endothelial, or angiogenic disorder in a mammal,
CC		preferably a human. The human may have suffered a myocardial infarction
CC		or has cardiac hypertrophy, trauma, a cancer, or age-related macular
CC		degeneration. The cardiac hypertrophy is characterised by the presence of
CC		an elevated level of BGP-2 alpha. A PRO polypeptide, given in the
CC		specification, or an agonist is used to inhibit or stimulate endothelial
CC		cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
CC		hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
CC		PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
CC		polypeptide, given in the specification, or an agonist is used to
CC		stimulate or inhibit smooth muscle cell growth, or to induce endothelial
CC		cell tube formation. The present sequence represents a cDNA encoding a
CC		PRO polypeptide of the invention.
XX		

SQ	Sequence	1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;	
	Query Match	39.0%; Score 422; DB 12; Length 1475;	
	Best Local Similarity	65.5%; Pred. No. 1.3e-116;	
	Matches	709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;	
QY	1	ATGGATAACTACACAGTGGCCCGGACGATGAATATATGATCTCTTAATCTTTAGACGACTAC	60
DB	29	ATGGCCAATTACACGCTGGACACGAGGATGAATGATGTCC---TCATAGAAGTGAA	85
QY	61	CTGGACAAAGTGGCCCGGACCAAGTT-----CCGCCCCCGAGTTCCTCTCCCCCAG	114
DB	86	CTGGAGAGCGATGAGGCAGAGCAATGTGACAAGTATGACGCCCGGCACTCTCAGCCCCAG	145
QY	115	CAGGTGCTGACAGTCTCTGCTGGGGGTGTTGGCGTGTCTCTTGGACACGTCCTGGCG	174
DB	146	CTGGTGCACATCTCTGCTCTGCTGTGTTGTGATGGTGTCTTGGACAATCTCTCGTGT	205
QY	175	GTGTTTATCTTGGTGAATAACAAGGACTCAAGAATCTGGGGAACATCTACTTCTCTAAAC	234
DB	206	GTGCTTATCTGTAAATATAAAGGACTCAACGCGTGGAAATATCTATCTTCTAAAC	265
QY	235	CTGGCACTTTCAAACTGTGTTCTCTGCTCCCTGCGGTTCTGGGCCCACTATCGACGA	294
DB	266	TTGGCAGTTTCTAACTGTGTTCTTGTCTTACCGCTGCGCTTCTGGGCTCATGCTG-----	320
QY	295	CACGGGGAAGCCCTGGCAAGGGACCTGTAAAGTTCTTTCGGACTCCCACTCTCTGGGC	354
DB	321	-----GGGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGTTGGGC	367
QY	355	TTATACAGCAGGTGTTTTCACATCTCTCTCTCTGTGCAAGATACAGGGGTGTTTTC	414
DB	368	CTGTACAGTGAGACATTTTTCATTTGCTTCTGACGTGCAAGGTACCTAGTGTGTTTG	427
QY	415	CAAGGGCGAC---TGGCCTCCATCTTCAACAGAGTGTCTTGTGATATTGTTGCGTCATC	471
DB	428	CACAAGGCAACTTTTCTCAGCCAGGAGGAGGTGCGCTGTGGCATCATTAAGTGTC	487
QY	472	CTGGCATGGCCATGGCTACTCGGCTCTCTTTCGCCGAGTCTGTGTTTATGACCTCG	531
DB	488	CTGGCATGGGTAAACAGCCATTCTGGCCACTTTGCTGCAATACGTGTTTATAAACCTCAG	547
QY	532	ATGGAAGACAGAAACAACAAGTGTGCTTTGGCAAACTCACTTCTTGGCAATCGAAGCG	591
DB	548	ATGGAAGACCAAGAAATACAAGTGTGCATTTAGCAGAACTCCCTTCTGCCAGCTGATGAG	607
QY	592	CCGCTCTGGAAGTACGTTCTGACGTCAAAAATGATCATCTTGTGACTGTCTTTTCTCTG	651
DB	608	ACATTTCTGGAAGCATTTTCTGACTTTAAAAATGAACATTTTCGGTCTCTTGTCTCCCTTA	667
QY	652	CTGGTTTTTATATCTGCTCGACCACTGAGGAGGAGGAGCTTCAGGGAGACAG	711
DB	668	TTTATTTTATCATTTCTATGTGCAAAATGAGAAAAACATAAGTTTCAGGGAGCAGAGG	727
QY	712	TACGACTCCACAAGCGGCTTGTGTCATAACGGCGTGTCTCTTTGTGTTGGGCGCT	771
DB	728	TATAGCTTTTCAAGCTGTTTGTGGCAATATGATGTCTCTCTGATGTGGGGGCC	787
QY	772	TACAACACTGTGCTTTTCTGCTCTGCTTTCCAGGAACACTTGTCTCCCTGCAAGGATGAGA	831
DB	788	TACAATATTGCATTTTCTGCTCCACTTTTCAAGAACACTTCTCTCTGAGTGACTGCAAG	847
QY	832	AGAGCTACCACTTGAACGCAAGTGTTCAGGTACACAGCTGTAGGACCACTCCACTGC	891
DB	848	AGCAGCTACAATCTGGACAAAAGTGTTCACATCACTAAATCTATGCCACCACTCCACTGC	907
QY	892	TGGCTCAACCGCTGCTCTATTGCTTCTTACCGGAAGGCCCTTTATGAGATACCTTCGC	951
DB	908	TGATCAACCCCTCTCTCTGATGCGTTTCTGATGGGA---CATTTAGCAATACCTCTGC	964
QY	952	AGCCTGTTCCACGGTGCAATGATATCCCTCTATCAAAAGTATGGAGGCTATCAGCAAGCG	1011
DB	965	CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGGCAGTCTGCACAAAGC	1024

Query Match
Best Local Similarity

39.0%; Score 422; DB 12; Length 1475;
65.5%; Pred. No. 1.3e-116;

QY 1012 CTCCCAAGGAGGTCTATGGAGGCCCATTTGACTGTACAGCAATTTGCATCAAGGCAG 1071
DB 1025 ACATCAGGGAAGAACCTGACCATTTCCCGAAGTGTAAACTAGCATCCACCAATGCAA 1084
QY 1072 GA 1073
DB 1085 GA 1086

RESULT 13
ADH43448

ID ADH43448 standard; cDNA; 1475 BP.

XX AC ADH43448;

XX DT 25-MAR-2004 (first entry)

XX Human PRO polynucleotide #8.

XX Human; PRO; gene; ss; cardiovascular disorder; endothelial disorder;
angiogenic disorder; endothelial cell growth; cardiac hypertrophy;
cell apoptosis; cell tube formation; angiogenesis;
smooth muscle cell growth; myocardial infarction; trauma; cancer;
age-related macular degeneration; cytostatic; cardiant;
cerebroprotective; ophthalmological; vulnery.

XX Homo sapiens.

XX US2003224984-A1.

XX PD 04-DEC-2003.

XX PF 26-NOV-2002; 2002US-00305654.

XX PR 20-JUN-2001; 2001WO-US019692.

XX (GETH) GENENTECH INC.

XX Baker KP, Ferrara N, Gerber H, Gerecht ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX WPI: 2004-042166/04.

XX P-PSDB; ADH43449.

XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful
PT for treating myocardial infarction, cardiac hypertrophy, trauma, cancer,
PT or age-related macular degeneration.

XX Claim 2; SEQ ID NO 15; 492pp; English.

XX The invention relates to human PRO polypeptides and the PRO
CC polynucleotides encoding them. The invention also relates to treating
CC cardiovascular, endothelial or angiogenic disorders in mammals,
CC inhibiting endothelial cell growth, stimulating endothelial cell growth,
CC inducing cardiac hypertrophy, cell apoptosis or cell tube formation and
CC stimulating angiogenesis or smooth muscle cell growth by administering
CC polypeptides of the invention. The PRO polypeptides and polynucleotides
CC are useful for treating cardiovascular, endothelial or angiogenic
CC disorders, e.g. myocardial infarction, cardiac hypertrophy, trauma,
CC cancer or age-related macular degeneration. The PRO polynucleotides are
CC useful as hybridisation probes in chromosome and gene mapping and in
CC generating antisense RNA and DNA, and for chromosome identification and
CC tissue typing. The PRO polypeptides and polynucleotides are also useful
CC in gene therapy and as molecular weight markers for protein
CC electrophoresis purposes. This sequence represents a human PRO
CC polynucleotide of the invention.

XX Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;

		Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;			
Qy	1	ATGATAACTACACAGTGGCCCGACGACGATGAATATGATGCTTAATCTTAGACGACTAC	60		
Db	29	ATGGCAATTTACACGCTGGCACGAGATGAATATGATGCTTCTTATGAGAGTGAA	85		
Qy	61	CTGGACAAAGTGGGCCGGAACAAGTT-----CGGGCCCGGAGTTCTCTCCGCCCCAG	114		
Db	86	CTGGAGAGCGATGAGGACAGACAAATGTGACAAGTATGACGCCCGGCACTCTCAGCCCGAG	145		
Qy	115	CAGGTGCTGCAAGTCTGCTGCGCGGTGTTGGGGTGGGTCTCTTGGACAAAGTGTGTCGG	174		
Db	146	CTGTGCGCATCACTCTGCTCTGCTGCTGTTGTGATTCGGTGTCTGTGACAAATCTCTCTGTT	205		
Qy	175	GTGTTTATCTTGGTGAATACAAAGGACTCAAGAATCTGGGGAACATCTACTTCTTAAC	234		
Db	206	GTGCTTATCTGTTAAATATTAAGGACTCAACCGGTGGAAATATCTATCTTCTTAAC	265		
Qy	235	CTGGCACTTTCAAACTGTGTTCTCTGCTTCCCTTCCCTGCGTTCTGGGCCCATACTGCAGCA	294		
Db	266	TTGGCAGTTTCTAACTGTGTTCTCTTACCTTCCCTTCTGGGCTCATGCTG-----	320		
Qy	295	CACGGGAAACCTCTGGCAAGCGGACCTGTAAAGTTCTTGTGGAATCTCACTCTCTGGGC	354		
Db	321	-----GGGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGTGGC	367		
Qy	355	TTATACAGGAGGTGTTTCCAAATCTCTCTCTCTGTCAGGATACAGGGTGTCTTCC	414		
Db	368	CTGTACAGTGAACATTTTCAATGTCCTTCTGACTGTGCAAGGACTCTAGTGTCTT	427		
Qy	415	CAAGGGCGAC---TGGCCTCCATCTTCACGACAGTGTCTGTGTATTGTTGGCTGCATC	471		
Db	428	CACAAGGCACTTTTCTCAGCAGGAGGAGGTGCCCTCTGCAATCATTTACAAGTGC	487		
Qy	472	CTGGCATGGCCATGGGCTAGTACGCGTCTCTTGTGCGGAGTCTGTGTTTATGAGCCTCGG	531		
Db	488	CTGGCATGGGTAACAGACCAATCTCGGCCACTTTGCTGAATACGTGGTGTATATAACCTCAG	547		
Qy	532	ATGAAAGACAGAAACACAGTGGCTTTGGCAAACTCACTCTTGGCAATCGAAGCG	591		
Db	548	ATGGAAGACCAAGAAATACAGTGTGCATTTAGCAGAACTCCCTTCTGCGCAGCTGATGAG	607		
Qy	592	CCGCTCTGGAAGTACGTTCTGACGCTCAAAAATGATCATCTTGTGTAATGTTTCTCTG	651		
Db	608	CAATCTGGAAGCAATTTCTGACATTTAAATGAACATTTGCGTCTTGTCTCCCTCCTA	667		
Qy	652	CTGTTTTTATAATCTGCTGCGGCAACTGAGGAGAGGAGAGCTTCAGGAGAGACAG	711		
Db	668	TTTATTTTACATTTCTATGTGCAATGAGAAAAACACTAAGGTTTCAGGAGCAGAGG	727		
Qy	712	TACGACCTCCACAGCGGCTTGTGATACGCGGCTGTTCTTGTGATGTTGGCGCCT	771		
Db	728	TATAGCCTTTTCAAGCTGTGTTTGGCCATAATGTAAGTCTTCTGATGTTGGCGGCC	787		
Qy	772	TACAACACTGTGCTTTCTGCTGCTTTCAGGAACACTTGTCTCCCTGCAAGATGAGAAG	831		
Db	788	TACATATGCAATTTTCTGCTGCTTTCAGGAACACTTCTCCCTGAGTGAAGTGCAG	847		
Qy	832	AGCAGCTACACCTGGACGCAAGTGTTCAGGTCAACAGCTGGTAGCGACACCCACTGC	891		
Db	848	AGCAGCTACATCTGGCAAAAGTGTTCACATCACTAACTCACTCGCCACCCCACTGC	907		
Qy	892	TGGTCAACCGCTGCTTATTTGCTTCTTGGACCGGAGGCTTTATGATAGTACCTTCG	951		
Db	908	TGCATCAACCTCTCTCTGATGCGTCTTGTGATGGA---CATTTAGCAATACCTCTGC	964		
Qy	952	AGCCTGTTTCCCAACGCTGCAATGATATCCCTTATCAAAAGTGTGAGGCTATCAGCAAGC	1011		
Db	965	CGCTGTTTCCATCTGCGTAGTAAACACCCCACTTCAACCCAGGGGGAGTCTGCAACAGC	1024		
Qy	1012	CTTCAAGGAGGTCTATGGCAGGCCCATTTGAATCTACAGCAATTTGCAATCAAGGCAG	1071		
Db	1025	ACATCGAGGGAAGAACTGACCAATTCACCGAAGTGTAAACTAGCATCCCAATGCA	1084		

Qy	1072	GA	1073		
Db	1085	GA	1086		
RESULT 14					
ADK82793					
ID	ADK82793 standard; cDNA; 1475 BP.				
XX	AC	ADK82793;			
XX	XX	20-MAY-2004 (first entry)			
DT	XX	Human PRO polynucleotide #8.			
DE	XX				
XX	XX	Human; PRO; gene; ss; cardiovascular disorder; endothelial disorder;			
KW	KW	angiogenic disorder; endothelial cell growth; cardiac hypertrophy;			
KW	KW	cell apoptosis; cell tube formation; angiogenesis;			
KW	KW	smooth muscle cell growth; myocardial infarction; trauma; cancer;			
KW	KW	age-related macular degeneration; cytostatic; cardiac;			
KW	KW	cerebroprotective; ophthalmological; vulnerary.			
XX	XX				
OS	OS	Homo sapiens.			
XX	XX	US2004043927-A1.			
PN	XX	04-MAR-2004.			
PD	XX				
PF	PF	20-FEB-2002; 2002US-00081056.			
XX	XX				
PR	19-SEP-1997;	97US-00933821.			
PR	23-JAN-1998;	98US-00015089.			
PR	10-SEP-1998;	98WO-US018824.			
PR	14-SEP-1998;	98WO-US019177.			
PR	16-SEP-1998;	98WO-US019330.			
PR	17-SEP-1998;	98WO-US019437.			
PR	19-NOV-1998;	98US-00180997.			
PR	01-DEC-1998;	98WO-US025108.			
PR	22-DEC-1998;	98US-00218517.			
PR	05-JAN-1999;	99WO-US000106.			
PR	12-FEB-1999;	99US-00214186.			
PR	03-MAR-1999;	99US-00254311.			
PR	08-MAR-1999;	99WO-US005028.			
PR	09-MAR-1999;	99US-00254460.			
PR	12-MAR-1999;	99US-00267213.			
PR	12-APR-1999;	99US-00284291.			
PR	02-JUN-1999;	99WO-US012252.			
PR	14-JUN-1999;	99US-00332928.			
PR	14-JUN-1999;	99US-00380137.			
PR	25-AUG-1999;	99US-00380138.			
PR	23-AUG-1999;	99US-00380139.			
PR	01-SEP-1999;	99WO-US020111.			
PR	08-SEP-1999;	99WO-US020594.			
PR	13-SEP-1999;	99WO-US020944.			
PR	15-SEP-1999;	99WO-US021090.			
PR	15-SEP-1999;	99WO-US021547.			
PR	05-OCT-1999;	99WO-US023089.			
PR	15-OCT-1999;	99US-00403154.			
PR	18-OCT-1999;	99US-00403296.			
PR	18-OCT-1999;	99US-00403297.			
PR	10-NOV-1999;	99US-00423741.			
PR	12-NOV-1999;	99US-00423843.			
PR	12-NOV-1999;	99US-00423844.			
PR	29-NOV-1999;	99WO-US028214.			
PR	30-NOV-1999;	99WO-US028313.			
PR	01-DEC-1999;	99WO-US028301.			
PR	01-DEC-1999;	99WO-US028634.			
PR	02-DEC-1999;	99WO-US028551.			
PR	02-DEC-1999;	99WO-US028564.			
PR	02-DEC-1999;	99WO-US028565.			
PR	16-DEC-1999;	99WO-US030095.			
PR	20-DEC-1999;	99WO-US030999.			

Db 608 ACAATCTGGAAGCATTTTCTGCATTTTAAATGAACATTTTCGGTTCTTGCTCTCCCCCTA 667
 Qy 652 CTGTTTTTAAATCTGTCGAGCACTGAGGAAGGAGAGCTTCAGGGAGAGACAG 711
 Db 668 TTTATTTTACATTTCTATGTGCAATGAGAAAAACACTAAGGTTTCAGGGAGCAGAG 727
 Qy 712 TACGACCTCCACAAGCGGCTCTGTCTATACCGGGCGTGTTCCTTTTGATGTGGCGGCT 771
 Db 728 TATAGCCTTTCAAGCTTGTCTTTCGCCATAATGTAAGTCTTCTGTATGTGGCGGCC 787
 Qy 772 TACAACACTGTGCTTCTGCTGCTTTCAGGAGACACTGTCTCCGCGCAGATGAGAG 831
 Db 788 TACAATATTGCAATTTTCTGCTGCACTTTCAAAGAACACTTCTCCCTGAGTACTGCAAG 847
 Qy 832 AGCAGCTACCACTGGAGCGAAGTGTTCAGGTTCACAGCTGTAAGCACCACCACTGC 891
 Db 848 AGCAGCTACAATCTGGACAAAGTGTTCACATCACTAACTATCGCCACCACCACTGC 907
 Qy 892 TGCCTCAACCGCTGCTCTATTGCTTCTTACCGGAAGGCTTTATGAGATACCTTGC 951
 Db 908 TGCATCAACCTCTCTGCTATGCGTTTCTTGATGGA---CATTTAGCAATACCTCTGC 964
 Qy 952 AGCTGTTCACCGTGCATGATATCCCTATCAAGTAGTGAGGCTATCAGCAAGCG 1011
 Db 965 CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGGCAGTCTGCACAAGC 1024
 Qy 1012 CTTCAAGGAGGTGATGCGAGCGCCATTGCACTGATGACCAATTTGCATCAAGGCGAG 1071
 Db 1025 ACATCGAGGAGAACTGACCAITCCACCGAAGTGTAACTAGCATCCCAATGCA 1084
 Qy 1072 GA 1073
 Db 1085 GA 1086

RESULT 15

ABZ42782
 ID ABZ42782 standard; DNA; 1645 BP.

AC ABZ42782;

XX 04-MAR-2003 (first entry)

XX Human chemokine receptor-like 2 nucleotide SEQ ID NO:353.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer; gene; ds.

XX Homo sapiens.

XX WO200261087-A2.

XX 08-AUG-2002.

XX 19-DEC-2001; 2001WO-US050107.

XX 19-DEC-2000; 2000US-0257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burner GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

DR P-PSDB; ABP81934.

XX

PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 (GPCR), useful for diagnosing and designing drugs for treating conditions
 in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 autoimmune diseases.

XX Disclosure, Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising: (a)
 any one of 1601 sequences (see ABP82019 to ABP83619) of 12-44 amino
 acids. Also described: (1) an assay for the detection of a particular G
 protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 and (2) an isolated antibody having high specificity and high affinity or
 avidity for a particular GPCR. (I) can be used as GPCR modulators and in
 gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 antibody against a particular GPCR, and in the production of specific
 antibodies. The peptides and antibodies are also useful for detecting the
 presence or absence of corresponding GPCRs. The antigenic peptides for
 GPCRs and antibodies are useful for diagnosing and designing drugs for
 treating immune-related diseases, growth-related diseases, cell
 regeneration-related disease, immunological-related cell proliferative
 diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 atherosclerosis, bacterial, fungal, protozoan or viral infections,
 osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 inflammation, allergies, Crohn's disease, diabetes, graft versus host
 disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 anxiety, depression, schizophrenia, dementia, mental retardation, memory
 loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or
 hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 any other disorder in which GPCRs are involved. The antibodies may be
 used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 GPCR proteins given in ABP81675 to ABP82018, which are used in the
 exemplification of the present invention

XX Sequence 1645 BP; 443 A; 383 C; 361 G; 458 T; 0 U; 0 Other;

Query Match 39.0%; Score 422; DB 8; Length 1645;

Best Local Similarity 65.5%; Pred. No. 1.3e-116;

Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;

Qy 1 ATGGATAACTACACAGTGGCCCGGACGATGATATGATGTCCTTAATTTAGACGACTAC 60
 Db 203 ATGGCCAATTACACGCTGGCCACGACGAGATGATGATGTCC---TCATAGAAGGTGAA 259
 Qy 61 CTGGACAACAGTGGCGCGACCAAGTT-----CCGGCCCCCGAGTTCCTCTCCCCCAG 114
 Db 260 CTGGAGAGCGATGAGGCGAGAGCAATGTGACAAGTATGACGCCCGGCACTCTCAGCCCG 319
 Qy 115 CAGGTGCTGCAGTTCTCTCGCGGCTGTTTGGCGGTCTCTTTGGACAACGTCGTGGCG 174
 Db 320 CTGGTGCATCACTCTGCTCTGCTGTTTGTGATCGGTGCTCTGGACAATCTCTGGTT 379
 Qy 175 GTGTTTATCTTGTGAATAACAAGGACTCAGAACTCTGGGAACATCTACTTCTTAAC 234
 Db 380 GTGCTTATCTCTGTAAATAATAAAGGACTCAAAACGCGTGGAAAAATATCTATCTTAAAC 439
 Qy 235 CTGSCACTTTCAAACTGTGTTCTCTCTTCCCTCGCGTTCCTGGGCCACTACTGCAGCA 294
 Db 440 TTGGCAGTTTCTAACTTGTGTTTCTTCTTACCCTGCCCTTCTGGGCTCATGCTG----- 494
 Qy 295 CACGGGAAAGCCCTGGCAACGGGACCTGTAAAGTCTTGTGCGACTCCACTCTCGGGC 354
 Db 495 -----GGGGCGATCCCATGTGTAAATTTCTCATTTGACTGTACTTCTGTGGC 541
 Qy 355 TTATACAGCAGGTGTTTTCACATCTCTCTCTTGTGCGAGGATACAGGGTGTCTTCC 414
 Db 542 CTGTACAGTGAGACATTTTTCATTTGCTTCTGACTGTGCAAGGTACCTAGTGTGTTG 601
 Qy 415 CAAGGGCGAC---TGGCCTCCATCTTCACGACAGTGTCTTGTGTTATTTGTCGTGATC 471
 Db 602 CACAAGGGCAACTTTTCTCAGCCAGGAGGGGTGCCCTGTGGCATCAITACAAAGTGC 661
 Qy 472 CTGGCATGGGCCCATGGCTACTGGGCTCTCTTTGCCCGAGTCTGTGTTTATGAGCCTCGG 531

[illegible]

Search completed: June 18, 2005, 07:10:42
Job time : 671.776 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 18, 2005, 06:34:54 ; Search time 637.224 Seconds
(without alignments)
9615.040 Million cell updates/sec

Title: US-10-623-472-31
Perfect score: 1035
Sequence: 1 atggcaattacacgtgcg.....accattccacgaagtgttaa 1035

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1035	100.0	1035	6	ABSS2092 Human CCR
2	1035	100.0	1547	2	AAV15419 Human mac
3	1035	100.0	1547	2	ABX95937 Human mon
4	1035	100.0	1547	12	ADQ67844 Human CDN
5	1032.2	99.7	1646	13	ADQ38349 Human SNP
6	1032.2	99.7	1776	13	ADQ38350 Human SNP
7	1031.8	99.7	1140	12	ACH89585 Human gen
8	1031.8	99.7	1475	6	ABL88079 Human pro
9	1031.8	99.7	1475	6	ABL95568 Human ang
10	1031.8	99.7	1475	10	ADD10304 Human sec
11	1031.8	99.7	1475	10	ADD11264 Human sec
12	1031.8	99.7	1475	10	ADD37057 Human sec
13	1031.8	99.7	1475	12	ADA41265 Human sec
14	1031.8	99.7	1475	12	ADH43448 Human PRO
15	1031.8	99.7	1475	12	ADK82793 Human PRO
16	1031.8	99.7	1645	8	ABZ42782 Human che
17	1031.8	99.7	1645	11	ADN95729 Human BEC
18	1031.8	99.7	1645	13	ADP24442 PRO polyp
19	1031.8	99.7	1645	13	ADS75309 Human CCR
20	1031.8	99.7	1698	12	ADP13564 Renal cel

21	1031.8	99.7	143040	11	ABD20648
22	1031.8	99.7	143067	11	ABD20815
23	1031.8	99.7	143068	3	AAA34983
24	1031.8	99.7	143068	3	AAA35150
25	1031.8	99.7	143068	3	AAF21272
26	1031.8	99.7	143068	3	AAF21105
27	1031.8	99.7	143068	3	ABL68124
28	1031.8	99.7	143068	6	ABT11034
29	1031.8	99.7	143068	10	ABZ96966
30	1031.8	99.7	143068	10	ABZ96799
31	1031.8	99.7	149412	3	AAA35151
32	1031.8	99.7	152739	11	ABD20816
33	1031.8	99.7	152740	3	AAF21273
34	1031.8	99.7	152740	10	ABZ96967
35	1030.2	99.5	1035	12	ADO30063
36	1029.8	99.5	1270	10	ACA56158
37	1029.8	99.5	1270	12	ADI55954
38	1029.4	99.5	1316	2	AAT99543
39	1028.8	99.4	1251	11	ADP03560
40	973.4	94.0	1050	2	AAV04641
41	973.4	94.0	1050	6	AAI17436
42	973.4	94.0	1050	6	AAI42836
43	695.8	67.2	7644	6	ABL32885
44	651	62.9	7644	6	ABL32884
45	505.2	48.8	588	5	AAF93267

ALIGNMENTS

RESULT 1
ABSS2092
ID ABS52092 standard; CDNA; 1035 BP.
XX
AC ABS52092;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human CCR12 CDNA.
XX
KW Human; CCR12; gene; ss; chemokine receptor; CCRAM-B; MCP-1; HEK cell;
KW Monocyte Chemoattractant Protein-1; brain glial cell; ischaemia; asthma;
KW inflammatory disease; degenerative brain disease; Alzheimer's disease;
KW multiple sclerosis; neurodegenerative disease; neuroinflammatory disease;
KW allergic encephalitis; chronic obstructive pulmonary disease;
KW obstructive airway disease; neuroprotective; antiinflammatory.
XX
OS Homo sapiens.
XX
WO200257779-A2.
XX
PD 25-JUL-2002.
XX
PF 18-JAN-2002; 2002WO-NL0000039.
XX
PR 18-JAN-2001; 2001EP-00200181.
XX
PA (UYGR-) RIJKSUNIV GRONINGEN.
XX
PI Boddeke BHWGM, Biber K;
XX
DR WPI; 2002-599725/64.
XX
PT Identifying compounds for treating inflammatory or degenerative brain
PT diseases, comprises testing the compound for its capacity to modulate or
PT mimic Monocyte Chemoattractant Protein-1 binding with a chemokine
PT receptor.
XX
PS Disclosure; Fig 8; 45pp; English.
XX
CC The invention relates to identifying a candidate drug compound comprising
CC testing the compound for its capacity to modulate or mimic Monocyte
CC Chemoattractant Protein-1 (MCP-1) binding with a chemokine receptor

CC capable of being expressed on brain glial cells and is known in the mouse
CC as L-CCR or in humans as CCR4-B. The chemokine receptor expressed in a
CC cultured cell comprising the cell transfected with a nucleic acid and a
CC HEK cell, is useful in identifying a candidate drug compound for treating
CC inflammatory or degenerative brain disease, e.g. ischaemia, Alzheimer's
CC disease or multiple sclerosis. The agonist or antagonist is useful in the
CC preparation of the pharmaceutical composition useful in treating
CC neurodegenerative and neuroinflammatory diseases such as allergic
CC encephalitis and chronic obstructive pulmonary disease and obstructive
CC airway diseases such as asthma. This sequence represents human CCR4-B
CC cDNA, also known as CCR12
XX
SQ Sequence 1035 BP; 255 A; 255 C; 228 G; 297 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 6; Length 1035;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCCAATTACACGCTGGCCACGAGGATGAATATGATGCTCTCATAGAAGTGAACCTG 60
DB |||||||
1 ATGCCCAATTACACGCTGGCCACGAGGATGAATATGATGCTCTCATAGAAGTGAACCTG 60
QY 61 GAGAGCGATGAGGAGGAGCAATGTGCAAGTATGAGCGCCAGGCACTCTCAGCCAGCTG 120
DB |||||||
61 GAGAGCGATGAGGAGGAGCAATGTGCAAGTATGAGCGCCAGGCACTCTCAGCCAGCTG 120
QY 121 GTGCCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB |||||||
121 GTGCCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 181 CTATCTCTGTAATAATATGAAGGACTCAAGCGGTGGAATAATCTATCTCTCTAAACTTG 240
DB |||||||
181 CTATCTCTGTAATAATATGAAGGACTCAAGCGGTGGAATAATCTATCTCTCTAAACTTG 240
QY 241 GCAGTTTCTAACTTGTGTTCTTCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB |||||||
241 GCAGTTTCTAACTTGTGTTCTTCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 301 CCATGTGTAATAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB |||||||
301 CCATGTGTAATAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 361 AATTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB |||||||
361 AATTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 421 GCCAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB |||||||
421 GCCAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 CTGGCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB |||||||
481 CTGGCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 541 TGTGCAATTTAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB |||||||
541 TGTGCAATTTAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 ACTTTAAATTTGAACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB |||||||
601 ACTTTAAATTTGAACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 661 GTGCAATTTAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB |||||||
661 GTGCAATTTAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 721 TTTGCGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB |||||||
721 TTTGCGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 781 TCCACTTTTCAAGAACTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB |||||||
781 TCCACTTTTCAAGAACTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840

QY 841 AGTGTTCACATCACTAACTCATCGCCACACCACTGCTGTCATCAACCCCTCTCTCTGTAT 900
DB |||||||
841 AGTGTTCACATCACTAACTCATCGCCACACCACTGCTGTCATCAACCCCTCTCTCTGTAT 900
QY 901 GCGTTTCTTGTATGGGACATTTAGCAAAATACCTCTGCGCTGTTTCCATCTGCGTAGTAAC 960
DB |||||||
901 GCGTTTCTTGTATGGGACATTTAGCAAAATACCTCTGCGCTGTTTCCATCTGCGTAGTAAC 960
QY 961 ACCCACTTCAACCCAGGGGGAGTGTGCAAGGACATCGAGGGAAGAACCTGACCAT 1020
DB |||||||
961 ACCCACTTCAACCCAGGGGGAGTGTGCAAGGACATCGAGGGAAGAACCTGACCAT 1020
QY 1021 TCCACCGAAGTGTAA 1035
DB |||||||
1021 TCCACCGAAGTGTAA 1035
RESULT 2
AAV15419
ID AAV15419 standard; cDNA; 1547 BP.
XX
AAV15419;
XX AC AC
XX 11-JUN-1998 (first entry)
XX
DE Human macrophage/dendritic cell chemokine receptor encoding cDNA.
XX
XX Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta; receptor;
KW dendritic cell; macrophage; inflammation; asthma; ss.
XX Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 49..1119
FT /tag= a
FT /product= "M/DC CR"
FT /note= "macrophage/dendritic cell chemokine receptor"
XX
PN W09801557-A2.
XX
PD 15-JAN-1998.
XX
XX 02-JUL-1997; 97NO-US010819.
XX
XX 05-JUL-1996; 96US-00675814.
PR 11-OCT-1996; 96US-0028329P.
PR 04-JUN-1997; 97US-0048593P.
XX
XX (SCHE) SCHERING CORP.
XX
XX Gish KC, Schall TJ, Vicari A, Zlotnik A, Wang W;
PI P-PSDB; AAW48087.
XX
XX WPI; 1998-101054/09.
DR
XX
XX Novel chemokines, e.g. thymus expressed chemokine - used for treating
PT inflammatory conditions including asthma.
XX
XX Claim 5; Page 95-97; 202pp; English.
XX
XX The present sequence encodes human macrophage/dendritic cell chemokine
CC receptor. Antibodies which bind to the protein can be used in detecting
CC or diagnosing various immunological conditions related to expression of
CC the protein. The nucleic acid can be used for screening and isolating DNA
CC clones for the chemokines, especially from other species. The chemokine
CC can be used in the treatment of conditions associated with abnormal
CC physiology or development, including inflammatory conditions such as
CC asthma
XX
SQ Sequence 1547 BP; 434 A; 357 C; 329 G; 427 T; 0 U; 0 Other;
Query Match 100.0%; Score 1035; DB 2; Length 1547;

Best Local Similarity 100.0%; Pred. No. 0;		Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	ATGCCCAATTACAGCTGGCCACGAGGATGAATATATGATCTCTCATAGAAGGTGAACCTG	60
Db	85	ATGCCCAATTACAGCTGGCCACGAGGATGAATATATGATCTCTCATAGAAGGTGAACCTG	144
Qy	61	GAGAGCGATGAGGAGGAGCAATGACAAAGTATGACGCCCGAGGACATCTCAGCCAGCTG	120
Db	145	GAGAGCGATGAGGAGGAGCAATGACAAAGTATGACGCCCGAGGACATCTCAGCCAGCTG	204
Qy	121	GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	180
Db	205	GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	264
Qy	181	CTTATCTCTGTAATAATAAAGGACTCAAAAGCGCTGGAAATATCTATCTTAAACTTG	240
Db	265	CTTATCTCTGTAATAATAAAGGACTCAAAAGCGCTGGAAATATCTATCTTAAACTTG	324
Qy	241	GCAGTTTCTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	300
Db	325	GCAGTTTCTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	384
Qy	301	CCCATGTGTAATAATCTCATTTGGACTGTACTTCTGCGGCTGTACAGTGAGACATTTTTC	360
Db	385	CCCATGTGTAATAATCTCATTTGGACTGTACTTCTGCGGCTGTACAGTGAGACATTTTTC	444
Qy	361	AATTGCCCTTCTGACTGTGCAAGGTACTAGTGTGTTTGGCAAGGGCAACTTTTCTCA	420
Db	445	AATTGCCCTTCTGACTGTGCAAGGTACTAGTGTGTTTGGCAAGGGCAACTTTTCTCA	504
Qy	421	GCCAGGAGGAGGGTGCCCTGTGGCATCAATCAAGTGTCTGGCATGGGTAACAGCCATT	480
Db	505	GCCAGGAGGAGGGTGCCCTGTGGCATCAATCAAGTGTCTGGCATGGGTAACAGCCATT	564
Qy	481	CTGCGCACTTTCCTGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	540
Db	565	CTGCGCACTTTCCTGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	624
Qy	541	TGTGCATTTAGCAAGTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	600
Db	625	TGTGCATTTAGCAAGTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	684
Qy	601	ACTTTAAATAATGAACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	660
Db	685	ACTTTAAATAATGAACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	744
Qy	661	GTGCAATATGAAAAACACTAAGGTTGAGGAGGAGGATAGCTTTTCAAGCTTGT	720
Db	745	GTGCAATATGAAAAACACTAAGGTTGAGGAGGAGGATAGCTTTTCAAGCTTGT	804
Qy	721	TTTGCCGTAAATGATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	780
Db	805	TTTGCCGTAAATGATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	864
Qy	781	TCCACTTTTCAAGAAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTCAATCTGCAAAA	840
Db	865	TCCACTTTTCAAGAAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTCAATCTGCAAAA	924
Qy	841	AGTGTTCATATCACTAAATCATGCCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	900
Db	925	AGTGTTCATATCACTAAATCATGCCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	984
Qy	901	GCGTTTCTGATGGGACATTTAGCAATACCTTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	960
Db	985	GCGTTTCTGATGGGACATTTAGCAATACCTTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1044
Qy	961	ACCCCACTTCAACCCAGGGGAGCTGTCGCAAGGACATCGAGGGAGAAACCTTGACAT	1020
Db	1045	ACCCCACTTCAACCCAGGGGAGCTGTCGCAAGGACATCGAGGGAGAAACCTTGACAT	1104
Qy	1021	TCCACCGAAGTGTA 1035	

Db	1105	TCCACCGAAGTGTA 1119
RESULT 3		
ABX95937		
ID	ABX95937	standard; cDNA; 1547 BP.
XX		
AC	ABX95937;	
XX		
DT	23-JUL-2003	(first entry)
XX		
DE	Human monocyte/dendritic cell receptor for chemokine (M/DC CR)	cDNA.
XX		
KW	Human; gene; ss; thymus expressed chemokine; TECK; chemokine; MIP-3alpha;	
KW	MIP-3beta; dendritic cell receptor for chemokine; DC CR; M/DC CR; asthma;	
KW	monocyte/dendritic cell receptor for chemokine; inflammatory condition;	
KW	abnormal physiology; abnormal proliferation; degeneration; atrophy;	
KW	antiinflammatory; antiasthmatic; cytostatic.	
XX		
OS	Homo sapiens.	
XX		
Key	Location/Qualifiers	
XX	49. .1119	
FT	CDS	
XX		
FT	/*tag= a	
XX	/product= "Human M/DC CR"	
XX		
PN	US2003018167-A1.	
XX		
PD	23-JAN-2003.	
XX		
PF	03-JAN-2002; 2002US-00039659.	
XX		
PR	05-JUL-1996; 96US-0021664P.	
XX		
PR	11-OCT-1996; 96US-0028329P.	
XX		
PR	04-JUN-1997; 97US-0048593P.	
XX		
PR	03-JUL-1997; 97US-00887977.	
XX		
PA	(SCHE) SCHERING CORP.	
XX		
PI	Wang W, Gish KC, Schall TJ, Vicari A, Zlotnik A;	
XX		
DR	WPI; 2003-416900/39.	
XX	P-PSDB; ABU09081.	
XX		
PT	New chemokines, TECK, MIP-3 alpha, MIP-3 beta, DC CR and M/DC CR, useful	
XX	for treating conditions associated with abnormal physiology or	
PT	development, including inflammatory conditions (e.g. asthma), and	
XX	abnormal proliferation.	
PS	Claim 4; Page 8-9; 54pp; English.	
XX		
CC	The invention relates to nucleic acids encoding the chemokines TECK, MIP-	
XX	3alpha, MIP-3beta, DC CR and M/DC CR. The polypeptide sequences are	
CC	useful in isolating DNA clones encoding the chemokines, for generating	
XX	antibodies, and for predicting oligonucleotides for screening a library	
CC	to isolate species variants. A nucleic acid encoding a chemokine	
XX	polypeptide can be used to identify genes, mRNA and cDNA species which	
CC	encode related or homologous ligands, as well as DNA encoding homologous	
XX	proteins from different species. The chemokines and antibodies which bind	
CC	to the polypeptides are useful in the treatment of conditions associated	
XX	with abnormal physiology or development, including inflammatory	
CC	conditions such as asthma, abnormal proliferation, regeneration,	
XX	degeneration and atrophy. This sequence represents cDNA encoding the	
CC	human monocyte/dendritic cell receptor for chemokine (M/DC CR)	
XX	polypeptide	
SQ	Sequence 1547 BP; 434 A; 357 C; 329 G; 427 T; 0 U; 0 Other;	
Query Match 100.0%; Score 1035; DB 10; Length 1547;		
Best Local Similarity 100.0%; Pred. No. 0;		
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	ATGCCCAATTACACGCTGGCCACGAGGATGAATATGATCTCTCATAGAAGGTGAACCTG 60

```
Db      85  ATGCCCAATTAACAGCTGGCCAGAGGATGATATGATGCTCTCATAGAGGTGAACG 144
Qy      61  GAGAGGATGAGGAGGAGCAATGTGACAGATATGAGCCGAGGCACTCTCAGGCCAGCTG 120
Db      145  GAGAGGATGAGGAGGAGCAATGTGACAGATATGAGCCGAGGCACTCTCAGGCCAGCTG 204
Qy      121  GTGCCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db      205  GTGCCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 264
Qy      181  CTTATCTCTGTAATAATATTAAGGACTCAAAACGGGTGGAATAATCTATCTTTAAACTTG 240
Db      265  CTTATCTCTGTAATAATATTAAGGACTCAAAACGGGTGGAATAATCTATCTTTAAACTTG 324
Qy      241  GCAGTTCTTAACCTGTTCTTCTGCTTAACCTGCTGCTTCTGCTGCTGCTGCTGCTGCTG 300
Db      325  GCAGTTCTTAACCTGTTCTTCTGCTTAACCTGCTGCTTCTGCTGCTGCTGCTGCTGCTG 384
Qy      301  CCATGTTGTAATAATCTCATTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db      385  CCATGTTGTAATAATCTCATTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 444
Qy      361  AATTGCTCTCTGACTGTGCAAAAGTACCTAGTGTGTTTTCACAAGGGCAACTTTTCTCA 420
Db      445  AATTGCTCTCTGACTGTGCAAAAGTACCTAGTGTGTTTTCACAAGGGCAACTTTTCTCA 504
Qy      421  GCAGAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db      505  GCCAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 564
Qy      481  CTGGCCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db      565  CTGGCCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 624
Qy      541  TGTGCTATTAGCAAGACTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db      625  TGTGCTATTAGCAAGACTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 684
Qy      601  ACTTTAAAAATGAACATTTTCGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db      685  ACTTTAAAAATGAACATTTTCGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 744
Qy      661  GTGCAATGAGAAACACTTAAGGTTTTCAGGAGGAGGATAGCTTTTCAAGCTTGT 720
Db      745  GTGCAATGAGAAACACTTAAGGTTTTCAGGAGGAGGATAGCTTTTCAAGCTTGT 804
Qy      721  TTTGCGCTAATGCTAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db      805  TTTGCGCTAATGCTAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 864
Qy      781  TCCACTTTCAAGAACACTTCTCCCTGAGTGTGCTGCAAGAGAGCTACAAATCTGGACAAA 840
Db      865  TCCACTTTCAAGAACACTTCTCCCTGAGTGTGCTGCAAGAGAGCTACAAATCTGGACAAA 924
Qy      841  AGTGTTCACATCACTAACTCATGCGCCACCAACCCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db      925  AGTGTTCACATCACTAACTCATGCGCCACCAACCCTGCTGCTGCTGCTGCTGCTGCTGCTG 984
Qy      901  GCGTTTCTCATGAGGACATTTAGCAATACCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db      985  GCGTTTCTCATGAGGACATTTAGCAATACCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1044
Qy      961  ACCCCACTTCAACCCAGGGGCGAGTCTGCAAGAGGACATCGAGGGGAAGAACTTGACCAT 1020
Db      1045  ACCCCACTTCAACCCAGGGGCGAGTCTGCAAGAGGACATCGAGGGGAAGAACTTGACCAT 1104
Qy      1021  TCCACCGAAGTGTA 1035
Db      1105  TCCACCGAAGTGTA 1119
```

```
ADQ67844
ID      ADQ67844 standard; cDNA; 1547 BP.
XX
AC      ADQ67844;
XX
DT      07-OCT-2004 (first entry)
XX
DE      Human cDNA encoding chemokine receptor M/DCCR.
XX
XX      Human; ss; gene; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW      chemokine receptor; DCCR; dendritic cell receptor for chemokine; M/DCCR;
KW      Monocyte/dendritic cell receptor for chemokine; abnormal physiology;
KW      development; inflammatory condition; asthma.
XX
OS      Homo sapiens.
XX
XX      Key Location/Qualifiers
FH      CDS 49..1119
FT      /*tag= a
FT      /product= "Human M/DCCR"
XX
PN      US2004137578-A1.
XX
PD      15-JUL-2004.
XX
XX      09-JAN-2004; 2004US-00754071.
XX
XX      05-JUL-1996; 96US-0021664P.
PR      11-OCT-1996; 96US-0028329P.
PR      04-JUN-1997; 97US-0048593P.
PR      03-JUL-1997; 97US-00887977.
PR      03-JAN-2002; 2002US-00039659.
XX
XX      (WANG/) WANG W.
PA      (GISH/) GISH K C.
PA      (SCHA/) SCHALL T J.
PA      (VICA/) VICARI A.
PA      (ZLOT/) ZLOTNIK A.
XX
PI      Wang W, Gish KC, Schall TJ, Vicari A, Zlotnik A;
XX
XX      WPI; 2004-533376/51.
DR      P-PSDB; ADQ67845.
XX
XX      New substantially pure or isolated Thymus Expressed Chemokine (TECK),
PT      useful for treating conditions associated with abnormal physiology or
PT      development, including inflammatory conditions, e.g. asthma.
XX
XX      Example 2; SEQ ID NO 11; 54pp; English.
XX
XX      The invention relates to a substantially pure or isolated polypeptide
CC      comprises the mature protein of human TECK (thymus expressed chemokine)
CC      whose full length sequence appears as ADQ67837. Also included are an
CC      isolated or recombinant nucleic acid encoding mature TECK, an expression
CC      vector comprising the nucleic acid, a host cell comprising the expression
CC      vector and a method for producing the polypeptide. Also disclosed are the
CC      mouse TECK cDNA and protein, human chemokines MIP-3alpha and MIP-3beta
CC      (and their encoding cDNAs), and the cDNAs and encoded proteins
CC      corresponding to human chemokine receptors DCCR (dendritic cell receptor
CC      for chemokine) and M/DCCR (Monocyte/dendritic cell receptor for
CC      chemokine). The polypeptide is useful for treating conditions associated
CC      with abnormal physiology or development, including inflammatory
CC      conditions, e.g. asthma. The present sequence encodes human chemokine
CC      receptor M/DCCR.
XX
SQ      Sequence 1547 BP; 434 A; 357 C; 329 G; 427 T; 0 U; 0 Other;
```

```
Query Match 100.0%; Score 1035; DB 12; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1  ATGCCCAATTAACAGCTGGCCAGAGGATGATATGATGCTCTCATAGAGGTGAACG 60
|||||
```


Db 328 ATGCCAATTRCACCTGGCACCAGAGGATGATGATGTCCTCATAGAGGTGAACCTG 387
Qy 61 GAGAGCGATGAGGACAGCAATGTGCAAGATATGACGCCAGGCACTCTCAGCCAGCTG 120
Db 388 GAGAGCGATGAGGACAGCAATGTGCAAGATATGACGCCAGGCACTCTCAGCCAGCTG 447
Qy 121 GTGCCATCACTCTGCTCTGCTGTTGTGATCGGTGTCCTGGACAATCTCTGTTGTG 180
Db 448 GTGCCATCACTCTGCTCTGCTGTTGTGATCGGTGTCCTGGACAATCTCTGTTGTG 507
Qy 181 CTATCTCTGTAATAAATATATAAGGACTCAAAACGCTGGAATAATCTATCTCTAACTTG 240
Db 508 CTATCTCTGTAATAAATATATAAGGACTCAAAACGCTGGAATAATCTATCTCTAACTTG 567
Qy 241 GCAGTTTCTAATCTGTTGTTCTGTTTACCTGCCCCCTCTGGCTCATCTGGGGCCGAT 300
Db 568 GCAGTTTCTAATCTGTTGTTCTGTTTACCTGCCCCCTCTGGCTCATCTGGGGCCGAT 627
Qy 301 CCCATGTGTAATAATCTCAATGGACTGTACTTGGTGGCCCTGTACAGTGAGACATTTTTC 360
Db 628 CCCATGTGTAATAATCTCAATGGACTGTACTTGGTGGCCCTGTACAGTGAGACATTTTTC 687
Qy 361 AATTGCCCTTCTGACTGTCAAAAGTACCTAGTGTGTTTTTTCACAAAGGCAACTTTTCTCA 420
Db 688 AATTGCCCTTCTGACTGTCAAAAGTACCTAGTGTGTTTTTTCACAAAGGCAACTTTTCTCA 747
Qy 421 GCCAGGAGGAGGTGCCCCCTGTGGCATATTACAAGTGTCTGGCATGGTAAACGCCATT 480
Db 748 GCCAGGAGGAGGTGCCCCCTGTGGCATATTACAAGTGTCTGGCATGGTAAACGCCATT 807
Qy 481 CTGGCCATTGTCCTGAATTCGTGTTTATATAAACCCTAGATGGAAGACCAAGATACAAG 540
Db 808 CTGGCCATTGTCCTGAATTCGTGTTTATATAAACCCTAGATGGAAGACCAAGATACAAG 867
Qy 541 TGTGCATTTACGAGAACTCCCTCTGCGCAGCTGATGAGACATTCGGAAGCATTTCTG 600
Db 868 TGTGCATTTACGAGAACTCCCTCTGCGCAGCTGATGAGACATTCGGAAGCATTTCTG 927
Qy 601 ACTTAAATAAAGCAATTCGGTCTCTGCTCCCTCTATTTATTTTACATTTCTCTAT 660
Db 928 ACTTAAATAAAGCAATTCGGTCTCTGCTCCCTCTATTTATTTTACATTTCTCTAT 987
Qy 661 GTGCAATGAGAAACCACTAAGGTTCAAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 720
Db 988 GTGCAATGAGAAACCACTAAGGTTCAAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 1047
Qy 721 TTTGCGTAAATGAGTCTCTCTGATGTGGGCGCCCTACATATTTGCAATTTTCTG 780
Db 1048 TTTGCGTAAATGAGTCTCTCTGATGTGGGCGCCCTACATATTTGCAATTTTCTG 1107
Qy 781 TCCACTTTCAAGAACACTTCTCCTGAGTGAAGTGAAGAGCAGCTACAAATCTGGACAAA 840
Db 1108 TCCACTTTCAAGAACACTTCTCCTGAGTGAAGTGAAGAGCAGCTACAAATCTGGACAAA 1167
Qy 841 AGTGTTCATCATTAATACTCATGCCACCAACCACTGCTGCATCAACCCCTCTCTGTAT 900
Db 1168 AGTGTTCATCATTAATACTCATGCCACCAACCACTGCTGCATCAACCCCTCTCTGTAT 1227
Qy 901 GCGTTTCTGATGGGACATTTAGCAATACCTCTGCGCGCTTTCCATCTCGTAGTAAC 960
Db 1228 GCGTTTCTGATGGGACATTTAGCAATACCTCTGCGCGCTTTCCATCTCGTAGTAAC 1287
Qy 961 ACCCCACTTCAACCCAGGGGCGAGTCTGCACAAAGCAGCATGAGGGAAGACCTGACCAT 1020
Db 1288 ACCCCACTTCAACCCAGGGGCGAGTCTGCACAAAGCAGCATGAGGGAAGACCTGACCAT 1347
Qy 1021 TCCACCGAAGGTAA 1035
Db 1348 TCCACCGAAGGTAA 1362

RESULT 7
ACH89585

ID XX ACH89585 standard; DNA; 1140 BP.
XX AC ACH89585;
XX DT 29-JUL-2004 (first entry)
XX DE Human genome derived single exon probe #22780.
XX KW Human; probe; ss; gene expression; single exon probe; microarray;
XX OS alternative splicing event; genomic alteration.
XX OS Homo sapiens.
XX PN US2003194704-A1.
XX PD 16-OCT-2003.
XX PF 03-APR-2002; 2002US-00029386.
XX PR 03-APR-2002; 2002US-00029386.
XX PA (PENN/) PENN S G.
XX PA (RANK/) RANK D R.
XX PA (HANZ/) HANZEL D K.
XX PI Penn SG, Rank DR, Hanzel DK;
XX WI MPI; 2004-119264/12.
XX PT New human genome-derived single exon nucleic acid probes useful for human
XX PT gene expression analysis, for identifying or characterizing alternative
XX PT splicing events, for assessing genomic alterations or as tools for
XX PT surveying tissues.
XX CC Claim 1; SEQ ID NO 22780; 80pp; English.
XX CC The invention relates to a nucleic acid probe for measuring human gene
XX CC expression, comprising any of the 27,400 fully defined nucleotide
XX CC sequences in the specification, or their complements or fragments, and
XX CC encoding at least 8 amino acids of any of the 688 amino acid sequences
XX CC fully defined in the specification. The probe is a single exon probe that
XX CC hybridises under high stringency conditions to a nucleic acid molecule
XX CC expressed in human cells or tissues. Also included are a spatially-
XX CC addressable set of single exon nucleic acid probes for measuring human
XX CC gene expression (comprising a plurality of single exon nucleic acid
XX CC probes cited above, where each of the plurality of probes is separately
XX CC and addressably isolatable or amplifiable from the plurality), a single
XX CC exon microarray for measuring human gene expression, a method of
XX CC measuring human gene expression, a vector comprising the single exon
XX CC probe cited above, an ORF-encoded peptide comprising at least 8
XX CC contiguous amino acids of any of the above-mentioned amino acid
XX CC sequences (optionally with conservative amino acid substitutions), an
XX CC isolated antibody that binds specifically to a peptide cited above,
XX CC methods of selling and/or licensing single exon probes or microarrays to
XX CC a customer desiring to measure gene expression, a method of providing
XX CC human gene expression data by subscription, and a computer-readable
XX CC storage medium which contains a database having a plurality of records
XX CC (each record including data on the expression of a single exon probe
XX CC cited above. The probe, methods and apparatus are useful in gene
XX CC expression analysis. The probes may be used as tools for surveying
XX CC tissues to detect the presence of expressed messages that contain their
XX CC specific exon, or in constructing genome-derived single exon microarrays.
XX CC In addition, the probes are used in identifying and characterising
XX CC alternative splicing events, in detecting and characterising gross
XX CC alterations in the genomic locus that includes their exon, in assessing
XX CC smaller genomic alterations, in priming the synthesis of nucleic acids,
XX CC or in expressing the ORF-encoded peptide. The present sequence is a human
XX CC single exon probe of the invention. Note: The present sequence is a human
XX CC patent did not form part of the printed specification, but was obtained
XX CC in electronic format directly from USPTO at
XX CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX SQ Sequence 1140 BP; 294 A; 275 C; 241 G; 330 T; 0 U; 0 Other;

Query Match		99.7%;	Score 1031.8;	DB 12;	Length 1140;
Best Local Similarity		99.8%;	Pred. No. 0;		
Matches 1033;		Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	ATGCCCAATTACACGCTGGCCACAGAGGATGAATAATGATCTCTCTCATAGAAAGTGAACTG 60			
Db	13	ATGCCCAATTACACGCTGGCCACAGAGGATGAATAATGATCTCTCTCATAGAAAGTGAACTG 72			
Qy	61	GAGAGCGATGAGGAGAGCAATGTGACAAGTATGACGCCCCAGGCACTCTCAGGCCAGCTG 120			
Db	73	GAGAGCGATGAGGAGAGCAATGTGACAAGTATGACGCCCCAGGCACTCTCAGGCCAGCTG 132			
Qy	121	GTGCCATCACTCTGCTCTGCTGTTTGTGATCGGTCTGCGACAAATCTCTGTTGTG 180			
Db	133	GTGCCATCACTCTGCTCTGCTGTTTGTGATCGGTCTGCGACAAATCTCTGTTGTG 192			
Qy	181	CTTATCTCGTAAATAATAAGGACTCAACCGGTGGAAATATCTATCTTCTAAACTTG 240			
Db	193	CTTATCTCGTAAATAATAAGGACTCAACCGGTGGAAATATCTATCTTCTAAACTTG 252			
Qy	241	GCAGTTTCTAACTGTTTCTGTTTACCTCGCCCTTCTGGGCTCATGCTGGGGGGAT 300			
Db	253	GCAGTTTCTAACTGTTTCTGTTTACCTCGCCCTTCTGGGCTCATGCTGGGGGGAT 312			
Qy	301	CCCATGTGTAATAATCTCATTTGACTGTACTCTGTTGGGCTGTACAGTGAGACATTTTTC 360			
Db	313	CCCATGTGTAATAATCTCATTTGACTGTACTCTGTTGGGCTGTACAGTGAGACATTTTTC 372			
Qy	361	AATTGCCCTCTGACTGTGCAAGGTACTAGTGTGTTTGGCACAAGGGCACTTTTCTCA 420			
Db	373	AATTGCCCTCTGACTGTGCAAGGTACTAGTGTGTTTGGCACAAGGGCACTTTTCTCA 432			
Qy	421	GCAGAGGAGGGTGCCCTGTGGCATCATTAACAAGTGTCTGGCATGGGTAAACAGCCATT 480			
Db	433	GCAGAGGAGGGTGCCCTGTGGCATCATTAACAAGTGTCTGGCATGGGTAAACAGCCATT 492			
Qy	481	CTGGCCACTTTGCTGAATTCGTGTTTATAAACCCTCAGATGGAAGACCAAGAAATCAAG 540			
Db	493	CTGGCCACTTTGCTGAATTCGTGTTTATAAACCCTCAGATGGAAGACCAAGAAATCAAG 552			
Qy	541	TGTGCATTTAGCAGAACTCCCTTCTGTCAGCTGATGAGACATTTCTGGAAGCAATTTCTG 600			
Db	553	TGTGCATTTAGCAGAACTCCCTTCTGTCAGCTGATGAGACATTTCTGGAAGCAATTTCTG 612			
Qy	601	ACTTTAAATATGAACATTTGCGTTCTTGCTCCCTCTATTTATTTTACATTTCTCTAT 660			
Db	613	ACTTTAAATATGAACATTTGCGTTCTTGCTCCCTCTATTTATTTTACATTTCTCTAT 672			
Qy	661	GTGCAATGAGAAACACACTAAGTTTCAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 720			
Db	673	GTGCAATGAGAAACACACTAAGTTTCAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 732			
Qy	721	TTTGCCGTAATGTTAGTCTTCTTCTGATGTGGGCGCCCTACAAATATTTGCAATTTTCTG 780			
Db	733	TTTGCCGTAATGTTAGTCTTCTTCTGATGTGGGCGCCCTACAAATATTTGCAATTTTCTG 792			
Qy	781	TCACATTTTCAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTACAATCTGGCAAA 840			
Db	793	TCACATTTTCAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTACAATCTGGCAAA 852			
Qy	841	AGTGTTCACATCACTAATCATGCGCCACCACTGCTGTCATCAACCTCTCTGTTAT 900			
Db	853	AGTGTTCACATCACTAATCATGCGCCACCACTGCTGTCATCAACCTCTCTGTTAT 912			
Qy	901	GCGTTCCTGATGGACATTTAGCAATACCTCTGCGCTGTTTCCATCTGCGCTAGTAAC 960			
Db	913	GCGTTCCTGATGGACATTTAGCAATACCTCTGCGCTGTTTCCATCTGCGCTAGTAAC 972			
Qy	961	ACCCCACTTCAACCCAGGGGGAGTCTGCAACAAGGCACATCGAGGGGAAGAACTTGACCAT 1020			
Db	973	ACCCCACTTCAACCCAGGGGGAGTCTGCAACAAGGCACATCGAGGGGAAGAACTTGACCAT 1032			

Qy	1021	TCCACCGAAGTGTA 1035
Db	1033	TCCACCGAAGTGTA 1047
RESULT 8		
ABL88079		
ID	ABL88079	standard; cDNA; 1475 BP.
XX	ABL88079;	
AC	ABL88079;	
XX		
DT	16-MAY-2002	(first entry)
XX		
DE	Human PRO1873	cDNA sequence SEQ ID NO:15.
XX		
KW	Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; Gene; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200200690-A2.	
XX		
PD	03-JAN-2002.	
PF		
XX	20-JUN-2001; 2001WO-US019692.	
XX		
PR	23-JUN-2000; 2000US-0213637P.	
PR	20-JUL-2000; 2000US-0219556P.	
PR	25-JUL-2000; 2000US-0220624P.	
PR	25-JUL-2000; 2000US-0220664P.	
PR	28-JUL-2000; 2000WO-US020710.	
PR	02-AUG-2000; 2000US-0223695P.	
PR	17-AUG-2000; 2000US-00643657.	
PR	23-AUG-2000; 2000WO-US023522.	
PR	24-AUG-2000; 2000WO-US023328.	
PR	07-SEP-2000; 2000US-0230978P.	
PR	18-SEP-2000; 2000US-00664610.	
PR	18-SEP-2000; 2000US-00665350.	
PR	24-OCT-2000; 2000US-0243922P.	
PR	08-NOV-2000; 2000US-00709238.	
PR	08-NOV-2000; 2000WO-US030952.	
PR	10-NOV-2000; 2000WO-US030873.	
PR	20-DEC-2000; 2000US-00747259.	
PR	20-DEC-2000; 2000WO-US034956.	
PR	22-JAN-2001; 2001US-00767609.	
PR	28-FEB-2001; 2001US-00796498.	
PR	28-FEB-2001; 2001WO-US006520.	
PR	01-MAR-2001; 2001WO-US006666.	
PR	09-MAR-2001; 2001US-00802706.	
PR	14-MAR-2001; 2001US-00808689.	
PR	22-MAR-2001; 2001US-00816744.	
PR	05-APR-2001; 2001US-00828366.	
PR	10-MAY-2001; 2001US-00854208.	
PR	10-MAY-2001; 2001US-00854280.	
PR	25-MAY-2001; 2001US-00866028.	
PR	25-MAY-2001; 2001US-00866034.	
PR	25-MAY-2001; 2001WO-US017092.	
PR	30-MAY-2001; 2001US-00870574.	
PR	30-MAY-2001; 2001WO-US017443.	
PR	01-JUN-2001; 2001WO-US017800.	
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;	
PI	Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;	
PI	Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;	

KW cardiovascular disorder; endothelial disorder; angiogenic disorder;
 KW myocardial infarction; cardiac hypertrophy; trauma; cancer;
 KW age-related macular degeneration; angiogenesis;
 KW endothelial cell apoptosis; smooth muscle cell growth;
 KW endothelial cell tube formation.
 XX Homo sapiens.
 OS
 XX
 PN US2003105011-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 16-AUG-2002; 2002US-00223084.
 XX
 PR 15-SEP-2000; 2000US-0232887P.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 20-FEB-2002; 2002US-00081056.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
 PI Watanabe CK, Williams PM, Wood WI, Ye W;
 XX
 DR WPI; 2003-810831/76.
 DR P-PSDB; ADD10305.
 XX

PT New isolated nucleic acid encoding a secreted and transmembrane
 PT polypeptide for treating a cardiovascular, endothelial, or angiogenic
 PT disorder in a mammal, such as cancer or age-related macular degeneration.
 XX
 PS Claim 2; SEQ ID NO 15; 493pp; English.

XX
 CC The invention relates to an isolated nucleic acid encoding a secreted and
 CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
 CC by the nucleic acid, or an agonist or antagonist, is used to treat a
 CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
 CC preferably a human. The human may have suffered a myocardial infarction
 CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
 CC degeneration. The cardiac hypertrophy is characterized by the presence of
 CC an elevated level of pG-2 alpha. A PRO polypeptide, given in the
 CC specification, or an agonist is used to inhibit or stimulate endothelial
 CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
 CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
 CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
 CC polypeptide, given in the specification, or an agonist is used to
 CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
 CC cell tube formation. The present sequence represents a cDNA encoding a
 CC PRO polypeptide of the invention.

XX
 SQ Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;

Query Match 99.7%; Score 1031.8; DB 10; Length 1475;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCCCAATTACAGCTGGCCACGAGGATGAATATGATGTCCTCATAGAGGTGAACCTG 60
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 29 ATGCCCAATTACAGCTGGCCACGAGGATGAATATGATGTCCTCATAGAGGTGAACCTG 88
 QY 61 GAGAGCGATGAGGAGAGCAATGTGACAAAGTATGACCGCCAGGCACTCTCAGCCGAGCTG 120
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 89 GAGAGCGATGAGGAGAGCAATGTGACAAAGTATGACCGCCAGGCACTCTCAGCCGAGCTG 148
 QY 121 GTGCCATCACTCTGCTGTGTTTGTGATCGGTGTCTGGACAATCTCTGTTGTG 180
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 149 GTGCCATCACTCTGCTGTGTTTGTGATCGGTGTCTGGACAATCTCTGTTGTG 208
 QY 181 CTTATCTCTGTTAAATATAAAGGACTCAAGCGCTGGAAATATCTATCTCTAACTG 240
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QY 241 GCAGTTTCTAACTGTGTGTTTCTTCTTACCTCGCCCTTCTGGGCTCATGCTGGGGGCGCAT 300
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 QY 301 CCCATGTGTAATAATTCATTTGGACTGTACTTCTGGGCTGTACAGTGAGACATTTTTC 360
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 329 CCCATGTGTAATAATTCATTTGGACTGTACTTCTGGGCTGTACAGTGAGACATTTTTC 388
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 449 GCCAGGAGGAGGTGCGCTTGTGGCATCATTAACAAGTGTCTGGCATGGGTAACAGCCATT 508
 QY 481 CTGSCCACTTTGCTGCAATTCGTGTTTATAAACTCAGATGGAAGACACAGAAATACAAAG 540
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 509 CTGSCCACTTTGCTGCAATTCGTGTTTATAAACTCAGATGGAAGACACAGAAATACAAAG 568
 QY 541 TGTGCATTTAGCGAAGTCTCCCTTCTGCGAGCTGATGAGACATTTCTGGAAGCATTTTCTG 600
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 569 TGTGCATTTAGCGAAGTCTCCCTTCTGCGAGCTGATGAGACATTTCTGGAAGCATTTTCTG 628
 QY 601 ACTTTAAATAATGAACATTTGCTGCTCTCCCTTATTTATTTTACATTTTCTCTAT 660
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 629 ACTTTAAATAATGAACATTTGCTGCTCTCCCTTATTTATTTTACATTTTCTCTAT 688
 QY 661 GTGCATAATGAGAAACACTTAAGTTTCAGGAGGAGAGGATATAGCCTTTTCAAGCTTGT 720
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 689 GTGCATAATGAGAAACACTTAAGTTTCAGGAGGAGAGGATATAGCCTTTTCAAGCTTGT 748
 QY 721 TTTGCCCTAATGAGTGTCTTCTTCTGATGTGGCGCCCTACAAATATTGCAATTTTCTCTG 780
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 749 TTTGCCCTAATGAGTGTCTTCTTCTGATGTGGCGCCCTACAAATATTGCAATTTTCTCTG 808
 QY 781 TCACATTTTCAAGAACACTTCTCTGAGTGTGCTGCAAGAGCAGTACAATCTGGAACAA 840
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 809 TCACATTTTCAAGAACACTTCTCTGAGTGTGCTGCAAGAGCAGTACAATCTGGAACAA 868
 QY 841 AGTGTTCACATCACTAACTCCTGCGCCACCCACCTGCTGCATCAACCTCTCTCTGAT 900
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 QY 901 GCGTTCCTGATGGGACATTTAGCAAAATACCTCTGCGCTGTTTCCATCTCGTAGTAAC 960
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 929 GCGTTCCTGATGGGACATTTAGCAAAATACCTCTGCGCTGTTTCCATCTCGTAGTAAC 988
 QY 961 ACCCACTTCAACCCAGGGGCGAGTCTGCAACAGGCAATCGAGGAGAAACCTGACCAT 1020
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 989 ACCCACTTCAACCCAGGGGCGAGTCTGCAACAGGCAATCGAGGAGAAACCTGACCAT 1048
 QY 1021 TCCACCGAAGTGTA 1035
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RESULT 11

ADD11264

ID ADD11264 standard; cDNA; 1475 BP.

XX AC

XX AC ADD11264;

XX AC

DT 01-JAN-2004 (first entry)

XX

DE Human secreted/transmembrane PRO polypeptide cDNA #8.

XX

KW ss; gene; human; secreted protein; transmembrane protein;

KW cardiovascular disorder; endothelial disorder; angiogenic disorder;

KW myocardial infarction; cardiac hypertrophy; trauma; cancer;

KW age-related macular degeneration; angiogenesis;

KW endothelial cell apoptosis; smooth muscle cell growth;

KW endothelial cell tube formation.

PD 05-JUN-2003.
 PF 16-AUG-2002; 2002US-00223088.
 PR 15-SEP-2000; 2000US-0232887P.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 20-FEB-2002; 2002US-00081056.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski BJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
 PI Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI; 2003-829354/77.
 DR P-PSDB; ADD37058.
 XX
 XX New isolated nucleic acids encoding a secreted and transmembrane
 PT polypeptide for treating a cardiovascular, endothelial, or angiogenic
 PT disorder in a mammal, such as cancer or age-related macular degeneration.
 XX
 XX Claim 2; SEQ ID NO 15; 492pp; English.
 XX
 CC The invention relates to an isolated nucleic acid encoding a secreted and
 CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
 CC by the nucleic acid, or an agonist or antagonist, is used to treat a
 CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
 CC preferably a human. The human may have suffered a myocardial infarction
 CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
 CC degeneration. The cardiac hypertrophy is characterised by the presence of
 CC an elevated level of PGF-2 alpha. A PRO polypeptide, given in the
 CC specification, or an agonist is used to inhibit or stimulate endothelial
 CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
 CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
 CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
 CC polypeptide, given in the specification, or an agonist is used to
 CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
 CC cell tube formation. The present sequence represents a cDNA encoding a
 CC PRO polypeptide of the invention.
 XX
 SQ Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;
 Query Match 99.7%; Score 1031.8; DB 10; Length 1475;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ATGSCCAATTACAGCTGGCCACGAGGATGAATATGATGTCCTCATAGAAGGTGAACCTG 60
 DB 29 ATGSCCAATTACAGCTGGCCACGAGGATGAATATGATGTCCTCATAGAAGGTGAACCTG 88
 QY 61 GAGAGCGATGAGGAGAGCAATGTGACAAGTATGACGCCAGGCACTCTCAGCCAGCTG 120
 DB 89 GAGAGCGATGAGGAGAGCAATGTGACAAGTATGACGCCAGGCACTCTCAGCCAGCTG 148
 QY 121 GTGCCATCACTCTGCTCTGCTGTGTTGTGATCGGTGTCTGGCAATCTCTCTGTTGTG 180
 DB 149 GTGCCATCACTCTGCTCTGCTGTGTTGTGATCGGTGTCTGGCAATCTCTCTGTTGTG 208
 QY 181 CTTATCTCTGGTAAATATAAAGGACTCAACCGGTGGAAATATCTATCTTCTAAACCTG 240
 DB 209 CTTATCTCTGGTAAATATAAAGGACTCAACCGGTGGAAATATCTATCTTCTAAACCTG 268
 QY 241 GCAGTTTCTACTGTGTTCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
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 QY 361 AATTGCCCTTCTGATGTGCAAGGTACTAGTGTGTTTGTGCAAGGGCAACTTTTCTCA 420

Db 389 AATTGCCCTTCTGATGTGCAAGGTACTAGTGTGTTTGTGCAAGGGCAACTTTTCTCA 448
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 QY 601 ACTTTAAAAATGAACATTTCTGTTCTCTCCCTATTATTTTATTTTACATTTCTCTAT 660
 Db 629 ACTTTAAAAATGAACATTTCTGTTCTCTCCCTATTATTTTATTTTACATTTCTCTAT 688
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 Db 689 GTGCAATGAGAAAAACACTAAGGTTCAAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 748
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 Db 749 TTTGCCAATATGGTAGTCTTCTCTGATGTGGGCGCCCTACAATATTGCAATTTTCTG 808
 QY 781 TCCACTTTCAAAGAACACTTCTCCCTGAGTGAATGTCGAAGAGCAGCTACAATCTGGACAAA 840
 Db 809 TCCACTTTCAAAGAACACTTCTCCCTGAGTGAATGTCGAAGAGCAGCTACAATCTGGACAAA 868
 QY 841 AGTGTTCACATCACTAACTCATGCCACCAACCCTGCTGATCAACCCCTCTCTCTGAT 900
 Db 869 AGTGTTCACATCACTAACTCATGCCACCAACCCTGCTGATCAACCCCTCTCTCTGAT 928
 QY 901 GCGTTTCTGATGGAGACATTTAGCAAAATACCTCTGCGGCTGTTTCCATCTCGTAGTAAC 960
 Db 929 GCGTTTCTGATGGAGACATTTAGCAAAATACCTCTGCGGCTGTTTCCATCTCGTAGTAAC 988
 QY 961 ACCCCACTTCAACCCAGGGGCGAGTCTGCAACAAGGCACATCGAGGGAAGAACCTGACCAT 1020
 Db 989 ACCCCACTTCAACCCAGGGGCGAGTCTGCAACAAGGCACATCGAGGGAAGAACCTGACCAT 1048
 QY 1021 TCCACCGAAGGTAA 1035
 Db 1049 TCCACCGAAGGTAA 1063
 RESULT 13
 ADE41265
 ID ADE41265 standard; cDNA; 1475 BP.
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 AC ADE41265;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human secreted/transmembrane PRO polypeptide cDNA #8.
 XX
 KW ss: gene; human; secreted protein; transmembrane protein;
 KW cardiovascular disorder; endothelial disorder; angiogenic disorder;
 KW myocardial infarction; cardiac hypertrophy; trauma; cancer;
 KW age-related macular degeneration; angiogenesis;
 KW endothelial cell apoptosis; smooth muscle cell growth;
 KW endothelial cell tube formation.
 XX
 OS Homo sapiens.
 OS
 PN US2003100497-A1.
 XX
 PD 29-MAY-2003.
 XX
 PF 16-AUG-2002; 2002US-00223085.
 XX
 PR 20-JUN-2001; 2001WO-US019692.
 PR


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PR 12-MAR-1999; 99US-00267213.
PR 12-APR-1999; 99US-00284291.
PR 02-JUN-1999; 99WO-US012252.
PR 14-JUN-1999; 99US-00333228.
PR 14-JUN-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 15-OCT-1999; 99US-0403154.
PR 18-OCT-1999; 99US-0403296.
PR 18-OCT-1999; 99US-0403297.
PR 10-NOV-1999; 99US-0423741.
PR 12-NOV-1999; 99US-0423843.
PR 12-NOV-1999; 99US-0423844.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005501.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 20-MAR-2000; 2000WO-US006884.
PR 15-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000WO-US030952.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 10-DEC-2000; 2000WO-US032878.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006566.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 05-APR-2001; 2001US-00828366.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
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PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.

PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 13-AUG-2001; 2001US-00929404.
PR 16-AUG-2001; 2001US-00941992.
PR 28-AUG-2001; 2001US-00946374.
PR 04-SEP-2001; 2001US-00948901.
PR 07-SEP-2001; 2001US-00948901.
PR 15-NOV-2001; 2001US-00002796.
PR 30-NOV-2001; 2001US-00001054.
PR 06-DEC-2001; 2001US-00006867.
PR 19-DEC-2001; 2001US-00028072.
PR 15-JAN-2002; 2002US-00052586.
PR 17-JAN-2002; 2002US-00053107.
PR 18-JAN-2002; 2002US-00052594.
PR 08-FEB-2002; 2002US-00072068.
PR 09-APR-2002; 2002US-00119480.
XX
XX (GETH ) GENENTECH INC.
PA Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PI Watanabe CK, Williams PM, Wood WI, Ye W;
XX
XX WPI: 2004-225727/21.
DR P-PSDB; ADK82794.
XX
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
XX Claim 2; SEQ ID NO 15; 494pp; English.
XX
XX The invention relates to human PRO polypeptides and the PRO
CC polynucleotides encoding them. The invention also relates to treating
CC cardiovascular, endothelial or angiogenic disorders in mammals,
CC inhibiting endothelial cell growth, stimulating endothelial cell growth,
CC inducing cardiac hypertrophy, cell apoptosis or cell tube formation and
CC stimulating angiogenesis or smooth muscle cell growth by administering
CC polypeptides of the invention. The PRO polypeptides and polynucleotides
CC are useful for treating cardiovascular, endothelial or angiogenic
CC disorders, e.g. myocardial infarction, cardiac hypertrophy, trauma,
CC cancer or age-related macular degeneration. The PRO polynucleotides are
CC useful as hybridisation probes in chromosome and gene mapping and in
CC generating antisense RNA and DNA, and for chromosome identification and
CC tissue typing. The PRO polypeptides and polynucleotides are also useful
CC in gene therapy and as molecular weight markers for protein
CC electrophoresis purposes. This sequence represents a human PRO
CC polynucleotide of the invention. Note: The sequence data for this patent
CC is also available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
XX Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;
SQ
Query Match 99.7%; Score 1031.8; DB 12; Length 1475;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGCCCAATTACAGCTGGCACCCAGAGGATGAATATGATGCTCTCATAGAGGTGAAGTCTG 60
Db 29 ATGCCCAATTACAGCTGGCACCCAGAGGATGAATATGATGCTCTCATAGAGGTGAAGTCTG 88
Qy 61 GAGAGCGATGAGCGAGAGCAATGTGCAAGATGAGCCCGAGCACTCTCAGCCAGCTG 120
Db 89 GAGAGCGATGAGCGAGAGCAATGTGCAAGATGAGCCCGAGCACTCTCAGCCAGCTG 148
Qy 121 GTGCCATCACTGCTCTGCTGTTGTGATCGGTGTCCTGACCAATCTCTCTGGTTGTG 180
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Qy 181 CTTATCTCTGGTAAATATATAAGGACTCAAAACGGTGGAAATATCTATCTTCTTAAGCTTG 240
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Qy      541 TGTGCATTTAGCAGAACTCCCTTCTGTCAGCTCATGAGACATTTCTGGAAGCATTTTCTG 600
Db      569 TGTGCATTTAGCAGAACTCCCTTCTGTCAGCTCATGAGACATTTCTGGAAGCATTTTCTG 628
Qy      601 ACTTTAAAAATGAACATTTGGTTCTTGTCTCCCTCTATTTATTTTTTACATTTCTCTAT 660
Db      629 ACTTTAAAAATGAACATTTGGTTCTTGTCTCCCTCTATTTATTTTTTACATTTCTCTAT 688
Qy      661 GTGCAATGAGAAJAAACACTAAGTTTCAGGGAGCAGAGGTATAGCCCTTTTCAAGCTTGT 720
Db      689 GTGCAATGAGAAJAAACACTAAGTTTCAGGGAGCAGAGGTATAGCCCTTTTCAAGCTTGT 748
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Qy      781 TCCACTTTCAAAGAACACTTTCTCCCTGAGTGACTGCAAGAGCAGCTACAATCTGGACAAA 840
Db      809 TCCACTTTCAAAGAACACTTTCTCCCTGAGTGACTGCAAGAGCAGCTACAATCTGGACAAA 868
Qy      841 AGTGTTCACATCACTAAACTCATGCGCCACCACTGCTGCTGCAATCAACCCCTCTCCTGTAT 900
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Qy      901 GCGTTTCTTGATGGGACATTTAGCAATACCTCTGCGCTGTTTCCATCTGCGTAGTAAC 960
Db      929 GCGTTTCTTGATGGGACATTTAGCAATACCTCTGCGCTGTTTCCATCTGCGTAGTAAC 988
Qy      961 ACCCACTTCAACCCAGGGGGAGTCTGCAAGGACATCGAGGGAAGAACCTTGACCAT 1020
Db      989 ACCCACTTCAACCCAGGGGGAGTCTGCAAGGACATCGAGGGAAGAACCTTGACCAT 1048
Qy      1021 TCCACCGAAGGTAA 1035
Db      1049 TCCACCGAAGGTAA 1063
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Search completed: June 18, 2005, 07:10:37
Job time : 646.224 Secs

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CC capable of being expressed on brain glial cells and is known in the mouse
CC as L-CCR or in humans as CCR4-B. The chemokine receptor expressed in a
CC cultured cell comprising the cell transfected with a nucleic acid and a
CC HEK cell, is useful in identifying a candidate drug compound for treating
CC inflammatory or degenerative brain disease, e.g. ischemia, Alzheimer's
CC disease or multiple sclerosis. The agonist or antagonist is useful in the
CC preparation of the pharmaceutical composition useful in treating
CC neurodegenerative and neuroinflammatory diseases such as allergic
CC encephalitis and chronic obstructive pulmonary disease and obstructive
CC airway diseases such as asthma. This sequence represents human CCR4-B
CC cDNA, also known as CCR12
XX
SQ

Sequence 1035 BP; 255 A; 255 C; 228 G; 297 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 6; Length 1035;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCCCAATTACAGCTGGACACAGAGGATGATATGATGCTCTCATAGAGGTGAAGCTG 60
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DB 121 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
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DB 721 TTTGCGGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 781 TCCACTTTTCAAGAGCACTTTCTCCCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 840
DB 781 TCCACTTTTCAAGAGCACTTTCTCCCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 840

QY 841 AGTGTTCACATCACTAAATCTATCGCCACACCCACTGTGTGATCAACCCCTCTCTGTAT 900
DB 841 AGTGTTCACATCACTAAATCTATCGCCACACCCACTGTGTGATCAACCCCTCTCTGTAT 900
QY 901 GCGTTTCTGATGGGACATTTAGCAATACCTCTGCGGCTGTTTCCATCTGCGTAGTAAC 960
DB 901 GCGTTTCTGATGGGACATTTAGCAATACCTCTGCGGCTGTTTCCATCTGCGTAGTAAC 960
QY 961 ACCCACTTCAACCCAGGCGGAGTCTGCAAGGACATCGAGGGAAGAACCTTGACCAT 1020
DB 961 ACCCACTTCAACCCAGGCGGAGTCTGCAAGGACATCGAGGGAAGAACCTTGACCAT 1020
QY 1021 TCCACCGAAGTGAAT 1035
DB 1021 TCCACCGAAGTGAAT 1035

RESULT 2

AAV15419

ID AAV15419 standard; cDNA; 1547 BP.

XX AAV15419;

AC AAV15419;

XX 11-JUN-1998 (first entry)

DT Human macrophage/dendritic cell chemokine receptor encoding cDNA.

DB Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta; receptor;

XX dendritic cell; macrophage; inflammation; asthma; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

PH 49..1119

FT /*tag= a

FT /product= "M/DC CR"

FT /note= "macrophage/dendritic cell chemokine receptor"

XX WO9801557-A2.

XX 15-JAN-1998.

XX 02-JUL-1997; 97WO-US010819.

XX 05-JUL-1996; 96US-00675814.

XX 11-OCT-1996; 96US-0028229P.

XX 04-JUN-1997; 97US-0048593P.

XX (SCHE) SCHERING CORP.

XX Gish KC, Schall TJ, Vicari A, Zlotnik A, Wang W;

XX WPI, 1998-101054/09.

XX P-PSDB; AAW48087.

XX Novel chemokines, e.g. thymus expressed chemokine - used for treating

XX inflammatory conditions including asthma.

XX Claim 5; Page 95-97; 202pp; English.

XX The present sequence encodes human macrophage/dendritic cell chemokine

XX receptor. Antibodies which bind to the protein can be used in detecting

XX or diagnosing various immunological conditions related to expression of

XX the protein. The nucleic acid can be used for screening and isolating DNA

XX clones for the chemokines, especially from other species. The chemokine

XX can be used in the treatment of conditions associated with abnormal

XX physiology or development, including inflammatory conditions such as

XX asthma

XX Sequence 1547 BP; 434 A; 357 C; 329 G; 427 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 1035; DB 2; Length 1547;

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Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	ATGGCCAAATTACACGCTGGCCACGAGAGATGAATGATGTCTCTCATAGAAAGGTGAACCTG	60
DB	85	ATGGCCAAATTACACGCTGGCCACGAGAGATGAATGATGTCTCTCATAGAAAGGTGAACCTG	144
QY	61	GAGAGCGATGAGGCGAGAGCAATGTGCAAGTATGACGCCCGAGGCACTCTCAGCCCGACCTG	120
DB	145	GAGAGCGATGAGGCGAGAGCAATGTGCAAGTATGACGCCCGAGGCACTCTCAGCCCGACCTG	204
QY	121	GTGCCATCACTCTGCTCTGCTGTGTTCTGTGATCGGTGTCCTGGAACATCTCTCTGGTTGTG	180
DB	205	GTGCCATCACTCTGCTCTGCTGTGTTCTGTGATCGGTGTCCTGGAACATCTCTCTGGTTGTG	264
QY	181	CTTATCTCTGTTAAATATAAAGGACCTCAAAACGCGTGGAAAAATATCTATCTCTTAAACCTG	240
DB	265	CTTATCTCTGTTAAATATAAAGGACCTCAAAACGCGTGGAAAAATATCTATCTCTTAAACCTG	324
QY	241	GCAGTTTCTAACTGTGTTTCTTGCTTACCTGCGCTTCTGGGCTCACTGCTGGGGCGCAT	300
DB	325	GCAGTTTCTAACTGTGTTTCTTGCTTACCTGCGCTTCTGGGCTCACTGCTGGGGCGCAT	384
QY	301	CCCATGTGTAAATTTCTCAATTTGGACTGTACTTCTGTGGGCTGTACAGTGAGACATTTTTC	360
DB	385	CCCATGTGTAAATTTCTCAATTTGGACTGTACTTCTGTGGGCTGTACAGTGAGACATTTTTC	444
QY	361	AAATGCCCTTCTGACTGTGCAAGGTACTAGTGTGTTTGTGCAAGGGCACTTTTCTCTCA	420
DB	445	AAATGCCCTTCTGACTGTGCAAGGTACTAGTGTGTTTGTGCAAGGGCACTTTTCTCTCA	504
QY	421	GCCAGGAGGAGGGTCCCTGTGGCATCAATTAACAAGTGTCTCTGGCATGGGTAAACAGCCATT	480
DB	505	GCCAGGAGGAGGGTCCCTGTGGCATCAATTAACAAGTGTCTCTGGCATGGGTAAACAGCCATT	564
QY	481	CTGGCCACTTGGCCCTGAAATTCGTGGTTTATAAACCAGATGGAAGACCGAAGATACAAG	540
DB	565	CTGGCCACTTGGCCCTGAAATTCGTGGTTTATAAACCAGATGGAAGACCGAAGATACAAG	624
QY	541	TGTGCATTTAGCAGAACTCCCTCTCCGACGTGATCAGACATTTCTGGAGCATTTTCTG	600
DB	625	TGTGCATTTAGCAGAACTCCCTCTCCGACGTGATCAGACATTTCTGGAGCATTTTCTG	684
QY	601	ACTTTAAAAATGAACAATTTGGTTCTTGTCTCTCCCTCTATTTATTTTATCAATTTCTCTAT	660
DB	685	ACTTTAAAAATGAACAATTTGGTTCTTGTCTCTCCCTCTATTTATTTTATCAATTTCTCTAT	744
QY	661	GTGCAAAATGAAAAACAATTAAGGTTGAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT	720
DB	745	GTGCAAAATGAAAAACAATTAAGGTTGAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT	804
QY	721	TTTGGCGTAATGTGTGTTCTTCTGATGTGGGCGCTTACAAATATGCAATTTTCTG	780
DB	805	TTTGGCGTAATGTGTGTTCTTCTGATGTGGGCGCTTACAAATATGCAATTTTCTG	864
QY	781	TCCACTTTCAAAGAACATTTCTCCCTGAGTGAATGCAAGAGCAGCTACATCTGGACAAA	840
DB	865	TCCACTTTCAAAGAACATTTCTCCCTGAGTGAATGCAAGAGCAGCTACATCTGGACAAA	924
QY	841	AGTGTTTCAATCACTAATCTATGCGCAACACCGACTGTGTCATCAACCTCTCTCTGTAT	900
DB	925	AGTGTTTCAATCACTAATCTATGCGCAACACCGACTGTGTCATCAACCTCTCTCTGTAT	984
QY	901	CGGTTTCTGATGGGACATTTAGCAATACCTCTGCGGCTGTTTCCATCTGGGTAGTAA	960
DB	985	CGGTTTCTGATGGGACATTTAGCAATACCTCTGCGGCTGTTTCCATCTGGGTAGTAA	1044
QY	961	ACCCCACTTCAACCCAGGGGCGAGTCTGCAACAAGGCACATCGAGGGAAGAACCTGACCAT	1020
DB	1045	ACCCCACTTCAACCCAGGGGCGAGTCTGCAACAAGGCACATCGAGGGAAGAACCTGACCAT	1104
QY	1021	TCCACCGAAGTGTA	1035

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